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Best Local Similarity
Matches 230; Conserv
                                                                      P70670; PRELIMINARY; PRT; 2187 AA.
P70670; PTGEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220).
 Mus musculus (Mousė).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Pred. No. 1
              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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FROM N.A.

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MEDITINE=96312450; PubMed=8698236;

A YOCOV W.V., St-Arnaud R.;

A YOCOV W.V., St-Arnaud R.;

RT info a muscle-specific transcription factor.";

RT info a muscle-specific transcription factor.";

RT Genes Dev. 10:1763-17721996).

DR EMBL; U48364; AAB18734.1; -.

DR EMBL; U48363; AAB18732.1; -.

DR MGDD, MGG:106095; NaCc.

DR InterPro; IPR002715; NAC.

DR InterPro; IPR003037; TS-N.

DR Pfam; PF01849; NAC; 1.

DR Pfam; PF02094; TS-N; 1.

DR Pfam; PF02094; TS-N; 1.
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Best Local Similarity 27.6%; Promatches 290; Conservative 119;
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LAE-SPSSPKK-APKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVS
                                                                                                                                LAPTITKEPTS-----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTT
                                                                                                                                                                                                                                                                                                                            VAGPKEASATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS-
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                                             LKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT
                                                                                                      TLVTPSSKKLSQTVGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTT
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Pred. No. 7.7e-
19; Mismatches
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hes 416;
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RESULT QUELT QUELT
RA Beeson K.Y. Benos P.V. Berman B.P. Bhandari D. Bolshakov S.R.
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Massaarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Massaarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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09VEL9;
01-MAY-2000 (TrE
01-MAY-2000 (TrE
01-JUN-2001 (TrE
CG4090 PROTEIN.
CG4090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRETPVTPAVPPVKNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPK 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPETP-----PPTTSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPK 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PTATSSGKDSHISPVS-DACSTGTTTP 1770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKVLMSSP-----PKKASSSKRASTLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAIN 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFPASPSIK-PVTT--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPA 1652
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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	1	ב אאכנהשהני גניביא זהשהני גהאסער שהערים - האנהשהני גניביאני שהערים אנו אליט (א. 2).	P	
	 T 17	CAPTIBEPTITSIPGYNPTITSVPGYNPTITPIPVETITSTPGYKPTTTGEPIT	_	
	T 652	600 PKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTST	Qy	
	7- 599 Y 1653	541 PTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPINTPKEPAPTTPKEPAPTT	Qy Db 1	
	- 1595	40 TTPSEESKDPGSTTPQSTDEPTTV	Db :	
	A 540	PAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTF	Qу	
	H	1480 GYMADDEDCRKYYRCINAGASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCSKLPAEDI	Db	
	NP 485	470EPAPTTPKKPA	Qy	
	E 14	PPTTTTGLPTTTTGAQPTTTTLSSETETSTVTTSPESTTQPPSTTTMKPLPAGTECT		
	469	421 PSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAP		
	SL 1419	70 TTPPPTTTDLPPTSTTGLP-PTTTTELPPT	당 성	
	T 13	VWDQDLQTCNHNFNNCSTGTESTTPKPPCEPATNGTTATSTS	Db Db	
	AP 360	4TKEPAPT	Qy	
	NK 1311	TARPVTARPT	DЬ	
	323	SAPTTPKEPAPTTKEF	Qy	
	 -р 1251	: :   :	Db	
	AP 290	EPASTTPKEPTPTTIKSAPTTPKEP	Qy	
	GT 1196	: : ::  :	Db	
	249	SAKDLAPTSKVLAKPTPKAETTTKGP	Qy	
	11	7 GSSNTGSSSNSGASSSGGSSNQGSSSNSGSSSGSNSSGNQSTSSSTSSSSSSSNNNN		
	EK 222	SLTVNKETTVETKETTTTNKOTSTDGKEKTTSAKETOSI	Qy	
	10			
	NS 175	116 KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPP	QУ	
	: QI 1028	: :   : :       : :	Db	
	RT 115	RGRECDCDAQCKKYDKCCPDYESFCAI	Qy	
47	Gaps	10.6%; Score 752; DB 5; Length 2112; tLocal Similarity 26.6%; Pred. No. 3.3e-42; ches 289; Conservative 105; Mismatches 356; Indels 338;	Que Bes Mat	
		SEQUENCE 2112 AA; 219547 MW; B91018E5551A5D36 CRC64;		
		o; IPR002557; Chitin_ o; IPR000561; EGF-lik r01607: Chitin hind 2	DR DR	
		EMBL; AE003716; AAF55402.1; - FlyBase; FBgn0038492; CG4090.		
		genome sequence of Drosophila melanogaster.		
	h н.о.,	W., Zhou X., Zhu S., Zhu X., Smit	R A	

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                                                                                                                                                                                                                                                              Query Match 10.1%;
Best Local Similarity 28.2%;
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9XDH2;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROLINE-RICH MUCIN HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1222; ATROPHIN.
PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO1218; PSTLEXTENSN.
SEQUENCE 763 AA; 75034 MW;
                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of a new member of the PGRS family that is a useful marker of polymorphism in Mycobacterium tuberculosis."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF071081; AAD41594.1; ... InterPro; IPR002951; Atrophin. InterPro; IPR002955; P_rich_extensn. InterPro; IPR003982; Pistil_extensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Espitia C., Laclette J.L., Mon Zhang Y., Moreno C., Singh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XDH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1930 -- CPETGP 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                              149
 470 TTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAP----TTTKKPAPTAPKEPAPTTPKETAP 525
                                                         412
                                                                                                                   358
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                                                                                                                                                                                                                                   238 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAP 297
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                                                                                    SRPALPPCPPPPVIPDPPEPAAPPVPPAPNSPPFPPFPPAPKFVPAPPVP--PVPNSPP 148
                                                                                                                                                                        TTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 357
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                            FPPFPPAALNPPAP----PAPPLANSPPLPPAPPTPAGT--PPAAPWPPVPAAPKSKPA 201
                                                                                                                                               PCP--PAP----PAPPKPKSKAPFPPVPPAPPARELAPPLP--PAP-----PEAPRE
                                                                                                                                                                                                      PVP-----APRALAPLPPAPPAPAEPKSKPPFPPAP-----PAPPCWMLVSAAP 46
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                                                         EP--APTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAP 469
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                                                                                                                                                                                                                                                              ; Score 715; DB 2; L; Pred. No. 3.5e-40; 39; Mismatches 361;
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                                                                                                                                                                                                                                                                                        Length 763;
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726 VPGAPLAPLPINGRPVFARKNSLIGSSSGDT 756	Db
972 TSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGET 1011	Qy
666 SMALPPAPPDPPIPLLATPPAPPAPPLPMSPPAPPLPPAAPDPPAPPLTINQPPSPPLAP 725	Db
921 SKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP 971	Qy
638 PAAPPAPPAPPVRATTP	Db
861 TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN 920	Qy
605PAPPAPPAPPSALPEVNPPA	Db
801 KEPGYPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI 860	Qy
549PAPPAPPTPPKLLSANPPCPPVPPAPNRPPAPPAPPAPPAPPELPAPPDPPTPPVANSP 604	ЪЪ
747 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSP 800	Qy
489 APPAPSMPSAVRVPPSPPIPPAPPAAPRASMPALPPAPPSPPATRLCPPLPPSPPAPNSP 548	Db .
694 KEPAPTTPKKPAPKELAPTTTKGP-TSTTSDKPAPTTPKETAPTTPKEPAPTTP 746	Qy
432PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP 488	Db ,
640 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTL 693	. VQ
374 TTTTPALPAPIPPLPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP 431	Dpp :
590TTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTP-KKPAPKE 639	Qy :
314 PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL 373	Db :
576PKAAAPNTPKEPAP 589	Qy
257 PVPNKIPPAPPAPPVAVAAVLVAPCPPLPPLPNNHPPAPPAAPVPGVPLAPLPNSHP 313	Db .
526 TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTT 575	0у
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Search completed: April 26, 2002, 16:30:35 Job time: 650 sec

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length: 2000000000
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2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
8: sp_organe1:
9: sp_phage:*
10: sp_plant:*
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
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Q9jlt1 rattus norv	057580 gallus gall	Q9n435 caenorhabdi	Q9fpq6 chlamydomon	Q9xdh2 mycobacteri	Q9vel9 drosophila	Q41805 zea mays (m	P70670 mus musculu	Q9lie8 arabidopsis	Q20007 caenorhabdi	Q9spm0 zea mays (m	096449 phytophthor	076894 drosophila	Q9i7s1 drosophila	Q9n4s7 caenorhabdi	077765 bos taurus	Q9jm99 mus musculu	Q9bx49 homo sapien	Q92954 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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Q91j64 arabidopsis	Q9sbm1 volvox cart	Q9nkc9 drosophila	Q27929 drosophila	Q99307 epstein-bar	Q23635 caenorhabdi	Q9n3y8 caenorhabdi	Q9rx57 deinococcus	001761 caenorhabdí	Q9xvs4 caenorhabd1	Q9zqi0 arabidopsis	Q17362 caenorhabdi	Q41707 vigna ungui	Q9vyq2 drosophila	w	Q9guw7 leishmania	Q9vc00 drosophila	Q14676 homo sapien	Q9qyx7 mus musculu	Q9qyx6 mus musculu	Q99552 homo sapien	Q23587 caenorhabdi	Q10465 homo sapien	Q94185 caenorhabdi	Q9vpg1 drosophila	Q9jks6 rattus norv

## ALIGNMENTS

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R SEQUENCE FROM N.A.

RA Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,

A Kelleher K., Glannotti J., Calvetti J., FitzGerald M., Kriz M.J.,

A Kelleher K., Glannotti J., Eraser H., Bean K., Norton C.R., Gesner T.,

RA Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T.,

RA Bhatla S., Kriz R., Hewick R., Clark S.C.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

DR EMBL; U70136; AAB09089.1; -.

DR InterPro; IPR000585; Hemopexin.

DR InterPro; IPR002400; GF_Cysknot.

DR InterPro; IPR002400; GF_Cysknot.

DR Pfam; PF00045; hemopexin; 2.

DR Pfam; PF00045; hemopexin; 2.

DR Pfam; PF01033; Somatomedin_B; 2.

DR PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92954 PRELIMINARY; PRT; 1404 AA. Q92954; Q92954; Q1-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-TUN-2001 (TrEMBLrel. 17, Last annotation update) 01-TUN-2001 (TREMBLICAL 17, Last annotation update) MEGAKARYOCYTE STIMULATING FACTOR.
                                                                                                                                                                                                                                                                                                       Mosher D.F. (eds.);
Biology of vitronectins and their receptors.,
Elsevier Science Publishers B.V. (1993).
                                                                                                                                                                                                                                                                                                                                                                    Merberg D.M., Fitz L.J., Temple P., FitzGerald M., Scaltreto J., Kelleh Jacobs K., Turner K.; (In) Preissner K.T., Rosenblatt S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.; Blood 78:279-279(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SEQUENCE 1404 AA; 151090 MW; AABD7A
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                                                                              KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT
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Pred. No. 0;
0; Mismatches
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	156 180	PPSGASOTIKSTTKRSPKPPNKKKTKKVIESEEITE	121	Qy Db	
	120 120	KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 	61	4d 4d	
	60	MAWKTLPIYLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 	<b>–</b>	Qy Db	
1;	ps	tch 99.4%; Score 7276.5; DB 4; Length 1404; al Similarity 96.7%; Pred. No. 0; 1358; Conservative 0; Mismatches 3; Indels 43; Ga	Query Ma Best Loc Matches	Z B O	
		SEQUENCE FROM N.A.  Wray P.;  Wray P.;  Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  EMBL; All33553; CAC36090.1;  SEQUENCE 1404 AA; 151076 MW; 782A11746B3FDEE5 CRC64;	SEQUI Wray Subm EMBL SEQUI	RP RA RL DR SQ	
		sapiens (Human). ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ryota; Butheria; Primates; Catarrhini; Hominidae; Homo. 	Homo Euka: Mamma NCBI	RN OCC	
		UN-2001 (TrEMBLrel. 17, Created) UN-2001 (TrEMBLrel. 17, Last sequence update) UN-2001 (TrEMBLrel. 17, Last annotation update) 4L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR ). 4L6.2.	01-JI 01-JI 01-JI 8G17	O D D D D D D D D D D D D D D D D D D D	
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	1260	KTEFEKDSQXWRETNDIKDAGYEKPIEKGEGGLTGQIYAALSTAKYKNWPESVY 	20	DP Q	
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	1157	DETNICNGKPVDGLTTLRNGTLYAFRGHYFWMLSPFSPDSPARRITEVWGIPSPIDTVFT	9	Qy	
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	0	OTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFWPEVTPDMDYLPRVPNOGIIINPMLS	03	νο	
	1037 1080	POKPTKAPKKPTSTKKPKIMPRVRKPKTPTPTRKMTSTMPELNPTSRIAEAMLOTTTRPN 	978 1021	DP QA	
	1020	TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEETAKPKDRATNSKATTPK	9	Db	
	977	TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPK	918	Qy	
	960	TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKLTATTTQV	901	Db	

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179 KSSKNSANRELQKNPNVKDNKKNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPDPPTT 238	Дb	
KPPVVDEAGSGLDNGDFKVT	Qy	
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MAWKTLPIYLLLLLSVFVIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 6	Qy	
uery Match 52.3%; Score 3826.5; DB 11; Length 1054; est Local Similarity 54.9%; Pred. No. 1.1e-245; atches 776; Conservative 59; Mismatches 167; Indels 411; Gaps	ឌី ណិហ៊	
PROSITE; PS00524; SOMATOMEDIN_B; 2. SEQUENCE 1054 AA; 115991 MW; 4FC64BFA42283235 CRC64;	SQ	
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Pfam; PF01033; Somatomedin_B; 2.	DR	
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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DYYAFSKDQYYNIDVPSRTARAITTRSGOTLSKVWYNCP 1361
                                                                                                                                                                                                                                                                                                              TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA
                                                                                                                                                                                                                                                                                                                                                                                                                RAIGPSQTHTIRIQYSPARLAYQDKGYLHNEVKYSILWRGLPNVVTSAISLPNIRKPDGY 1322
                                                                                                                                                                                                              ALSIAQYKSRPESVYFFKRGGSVQQYTYKQEPTQKCTGRRPAINYSVYGETAQVRRRRFE
                                                                                                                                                                                                                                      ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFE 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1082
                                                                                                       RAIGPSQVHTIRIHYTPVRVPYQDKGFLHNEVKVSTLWRGLPNVVTSAISLPNIRKPDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-LPEAMLQTTTRPTPTPNSEIIDVNSENEDGDAAEGEKPHMIFRPPVLTPIVIPGTEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1713.5; DB 6; Pred. No. 4.8e-106; 24; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86147CC9AFBB73D7 CRC64;
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Best Local Similarity
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AC006797; AAF60743.1; -
InterPro; IPR002965; P_iich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
85001ENCE 1079 AA; 110532 MW; 8DBDE3824CF8
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. eleg
Submitted (MAR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. Y51B11A.1 PROTEIN. Y51B11A.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cotton M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
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                                                                                                                                                                                TPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAP--TTTKEPAPTTTKSAPTTPKE
                                                                                                                                                                                                                                                                                     PAPTTPKKPAPTTPKEPAPTTPKEPAPTTKEPAP-TTPKEPAPTAPKKPAPT |:: | || || || :: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAKDLAPTSKVLAKPTPKAETTTKGP--ALTTPKEPTPTTPKEPASTTPKEPIPTTIKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSTLTSVDME----TPSTLVLSSTPTSSSTPIKETTTTAP------ETTS
                                                                                                                                                                                                                                                                                                                                                            TTTAPETTSTESPSSSTTPVQTTTTTAPE---TTSTEP-PSSSTTPVQTTTTTAPETTST
                                                                                                                                                                                                                                                                                                                                                                                            TEPPSSSTTPVQTT - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSP-KITTAKPI
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  PTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP--TPTTPEEPAPT 624
                                                  PETTSTEPPSSST--TPVQTTTITAPETTSTEP-PSSSTTPVQTTTTTAPETTSTEPPSS
                                                                                 PSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEP--A
                                                                                                                                                      TPVQTTTTT----APETTRTEPPSSSTTPVQNTTTTAPETTSTEPPSSSTTPVQTTTTTA
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28.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 982; DB 5;
%; Pred. No. 4.2e-57;
151; Mismatches 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmid Y51B11A.";
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501;
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Дb	
Qy	TTPKEPAPTTPKEPAPTTPKET
Db	PVQTTTTTAPETTSTEPPSSS-TTPVQTTTTTAPETT
Qy	-APTTPKGTAPTTPKEPAPTTPKEPAF
Db	571 PPSSSTTPVQTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQT 627
Qy	TTPK 7
В	628 TTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEP- 686
Qy	TPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKE
Db	687PSSSNTPVQTTTTTAPETTSTEPPSSSTSPVQTTTTTAPETTSTEPPSSST 737
Qy	PETTTAAPKMTKETATTTEKTTES
В	PVQTTTITAPETTSTEPPSSSTTPVQTT
Qy	TTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETA-KPKDRAT
рь	EPPSSSTSPVQTTTITAPETTSTEPPSSSNTPVQTTTTTAF
Ωу	KPTSTKKPKTMPRVRKPKTTPTPRKM
Db	854 PVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPET 911
Qy	TRPNQTPNSKLVEVNPKSEDAGGAEG-ETPHMLLRPHVF
Ф	912 -TSTEPPSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTVPCDCSLSYIDRVV 967
Qy	
Db	IIQSYDSPRRTAFSFVSTFDIGTCTAILTCIYTSEGGISNL-NA
Qy	1120 VAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVETRCNCEGKTFFFKDSQ 1172
Db	GLE-IMPEINC
Qy	1173 YWRFTN 1178
Db	1060 -WSYNN 1064
su 17	
	(TrEMBLrel. 16, Created)
	(TrEMBLrel. 16, Last se (TrEMBLrel. 17, Last an
	melanogaster (Fruit fly). Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
288	а; Endopterygota; Diptera; Bracnyce philidae; Drosophila.
	ELEY;
	Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.
	P.G., Scherer S.E., Li P.W., Hoskins R.A., (
	, Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Rogers YH.C., Blazel R.G., Champe M., Pfeiffer B.
	oyle Ĉ., Baxter E.G., Helt G., Nelson C.R., Miklos G. Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin

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RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup F., Gorrell J.H., Gu Z., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mcinton G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcinton S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Spier E., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeld, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhon W., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Globas R. A., Wyers E. W., Ruber J., Shan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng X.H., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Sheng X.H., Wassarman D.A., Weinstock G.M., Wassarma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.0
Best Local Similarity 35.1
Matches 376; Conservative
                                                     422
562 PKEPAPTTPKETAPTTPKKLTPTTPEKLAPT--TPEKPAPTTPEE----LAPTT--PEEPT 614
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                                                                                                                                                                        TAPKKPAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKSAPTTTKEPAPTTTKS
                                                                                          APTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTA
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                                              -PTEGTTAKPTTLKPTEGTTAK---PTTLK---PTEGTSAKPTTLK-PTEGTTAKPTTLK
                                                                                                                                           TEGTSAKPTTLKPTEGTTAK---PTTLK---PTEGTSAKPTTLKPTEGTTAK--PTTLK-
                                                                                                                                                                                                                                     TTLK----PTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTDGTTAKPTTLKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTS--TTQHNKVSTSPKITTAKPINPRPSLPP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 955; DB 5; Length 1049; 35.1%; Pred. No. 2.5e-55; Live 54; Mismatches 474; Indels 168;
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avenport L.B., Davies P., ays A.D., Dew I., Dietz S.M	J.M., Cawley S., Dahlke bs B., Delcher A., Deng	Cherry de Pab	RA RA
yraktarogiu L., Beas Bhandari D., Bolsha Okstein P., Brottie dieu E., Center A.,	(.Y., Benos P. D., Botchan N	K H @ F	RA RA
.G., Champe M., Pfeiffer E G., Nelson C.R., Miklos G. rews-Pfannkoch C., Baldwir	R.C., Rogers YH, Doyle C., Baxter .F., Agbayani A., A	Brandon Wan K.H Abril J	RA RA
, Hoskins R.A., Galle Ashburner M., Henderso ., Zhang Q., Chen L.X.	des P.G., Sche R.A., Lewis S. G.G., Wortman	Amana Georg Sutto	RA RA
., Evans C.A., Gocavne J.D	(ELEY; 196006; PubMed=1 Celniker S.E.,	STRAIN= MEDLINE Adams M	RRC
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sophila.	Neoptera; Endo 1; Drosophilida 17227:	Ephy	288
a; Hexapoda; Insecta;	la melanogast a; Metazoa; <i>P</i>	Euka	200
	OR CG14796.	E E E	0 N
<pre>:ed) sequence update) annotation update)</pre>	998 (TIEMBLIEL. 08, Creat 999 (TIEMBLIEL. 12, Last 090 (TIEMBLIEL. 17, Last		
,	PRELIMINARY; PR	700	18 I S I
PTTLKPTKGTSGQANNFETKRKERRP 1045	TLKPTERTSAQPTTLKPTEGTTAK	996	В
NQTPNSKLVEVNPKSEDAGGAEG-ETPHMLLRP 1068	ELNPTSRIAEAMLQTTTRP	1018	Qy
TAKPTTLKPTEGPSAKPTTLKPTERTSAQPT	-GTTAKPTTLKPTEGTSAKPTTLKPTEG	937	Db
STKKPKTMPRVRKPKTTPTPRKMTSTMP-	RATNSKATTPKPQKPTKAPKKPT	967	Qy
TTLKPTDGTTAKPTTLKPTEGTSAKPTTLKPTE	PTTLKPTEGTSAKPTTLKPTEGTTAKP	877	Db
LAPKVTTTKKTITTTEIMNKPEETAK	KITATTTQVTSTTTQDTTPFKITTLKT	909	Qγ
ETTTAAPKMTKETATTTEKTTES	PEMTTTAKDKTTERDLRTT	866 817	Дb
SAQPTTLKPTER	TLKPTEGTSAKPTTLKPTEG	762	뫄
KALENSPKEPGVPTTKTPAATK	- 13	825	Qy
TSAKPTTLKPTEGTTAKPTTLKPTEGTRTTAKPT	TSAKPTTLKPTEGTTAKPTTLKPTEG	702	Дb
TTPKKPAPTTPETPPPTTSEVSTPT-TTKEPT	TSDKPAPTTPKETAPTTPKEPAP	771	δõ
  TEGTTAKPTTLK	EGTTAKPTTLKPTEGTSA	648	Д
APTTLKEPAPTTPKKPAPKELAPTTTKGPTST	APTTPKEPAPTTPKEPAPTTPKGT/	715	Qy
		591	Дb
TKEPTSTTSDKPA	TLKEPAPTTPKKPAPKI	673	Qγ
EGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPT	:        TAKPTTLKPTEGTSAKPTTLKPT	534	Db
KEPAPTTPKEPAPTTPKETAPTTPKGTAPT	5 PTTPEEPAPTTPKAAAPNTPKEPAPTTP	615	Qy
PTEGTTAKPTTLKPTKGTXGTSAKPTTLKPTEGTTAKPTTLKPTEGTTAKPTTLKPTKGT		474	DЬ

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Best Local Similarity
Matches 281; Conserv
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EMBL; AL031028; CAA19845.2; ...
FlyBase; FBgn0025390; EG:56G7.1.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; Chitin_bind_2; 2.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cadieu E., Dreano S., Lelaure V., Mottler S., Galibert F.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Cadieu E., Dreano
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1999)
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PAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPK-----
                                                                                                                                                                                                       TTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDT-----SKETSLTVNKET
                                                                                                                                                                                                                                                     STTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKV
                                          STTTPSTTTPST-----TTPSTTTPST-----TTPSTTTPSTTTTVKVSTHRPRTTSQK
                                                                                                                                                                                                                                   ATTREPLNDINKYOYKRYTYGTD-----KNDVTEAPEIKSPL----KGLHLSENIV 454
                              TTTEKTSTVSTTTKKSTESSPKPTSSTGKPTTTPKPSTRTTPTTTKVTTTTQITTTTPLR
                                                                       TTTASTTTKK---
                                                                                                                               ALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTK 359
                                                                                                                                                    TTTKRPTTVTEKTSSATEKPRTTVVTTTTQKRSTTTHNTSPDTKTTIRSTTLSPKTTTTP
                                                                                                                                                                        TVETKETTTTNKOTSTDGKEKTTSAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGP
                                                                                                                                                                                           ILPETTTT--TTTTTKPVVLTCPTISPPDTTPKPSTTTAVTKSTPKISSTEQHSTTTAKT
                                                                                         - EPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP
                                                                                                                                                                                                                                                                           Conservative
                                                                      -TTTSPKTTKTTDIPTSTTSKLSTTTQKTTTTTHKFTAATTSTEKPK
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Pred. No. 2.4e
.34; Mismatches
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2.4e-49;
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ğ i	9	TKVAITTQKETTPTQSTSTIFTRKTTTNNPEPTSTEKPITSTTPKPSTTTPKTSTVAS 85
Ϋ́	577	KLIPITPEKLAPITPEKPAPITPEELAPITPEEPTPITPEEPAPITPKA 6
ŏ	858	STEKTTISSPKPTTEKSTENPTTNSVKTSALTSSTQRATSTTSEPTKTT-QNITTTTPKP 916
Ϋ́	629	AAPNTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPA 686
ŏ	917	TTLKTSTQEATTSTQKVSTVTITTKKATESSPLTTLSTEEPNTTPKPLRTTTPTTTSVTA 976
Ϋ́	8	ELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPK :       : : :                  :
ŏ	977	I.S
Ϋ́	745	EPAPTTPKKPAPKELAP-TTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTT 803
ŏ	1036	STQRETTTTRQETSITASTTSIGTTRIPTTNPQNSTS
γ̈́	804	SEVSTPTT-TKE
ŏ	1091	ğ.
Ϋ́	844	KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKET
ŏ	1151	TMSTLAAAHLLQKLFHIISTTPPSREHAPT
Ϋ́	901	TTEKTŢESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMN 956
ŏ	1209	-GVTTAQMARHNLATSKPFTAHSLRLSTQQLASTQKRSTPPKT
γ	957	KPKDRATNSKATTPKPQKPTKA-PKKPTSTKKPK
ŏ	1268	PED-SEYYDSETSEQYTDEDNEVLDKTQPRAMSSTTVAAVLPAVPSTTTEREP
γ	1016	MPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSED 1053
ŏ	1326	SPSPTKATSSTTTQPIETTTGDLEYDSSGSSD 1357
ESUL?	Ei Qu Qu	
	096449 096449;	PRELIMINARY; F
		1999 (TrEMBLrel. 10, Created) 1999 (TrEMBLrel. 10, Last sequence updat,
	CYST	Y-1999 (TrEMBLrel. 10 GERMINATION SPECIFIC
	CAR90. Phytopht	chora infestans (Potato late blight fungus)
ממ	Eukaryot Phytopht	a; stramenopiles; Oomycetes; Pythiales; p
	[1] NCBT	(TD=4/8/;
	SEQUENC STRAIN-	NCE FI
	Goern Submi	hardt B.; tted (APR-1998) to t
	SEQUI	1489 AA; 1
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Bes	ery Ma	al Similarity 32.2%; Pred. No. 2.5e-49;
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1365 TDEPTDEPTDE--PSDEPTDEPTDLPTDEPSTPCDNQGINGIGVENKVRYNNAG 1420
                                      1000 VRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP--NQTPNSKLVEVNPKSEDAG 1055
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                                                                                                      NKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT------STKKP-KTMPR 999
                                                                                                                                                             TTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEETTYAPTEATTYAPTEETPYA 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPAPT-TTKSAPTTPKEPAPT--TTKEPAPTTPKEPAPTTTKEPAPTTTKSAPT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-----APT-TTKSAPT-----TTKEP----APT-TTKSAPT--TPKEPSPT 512
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                                                                                 PTEETTYEPTGETTYAPTEETTYAPTEETTYAPMEETPYEPAEESTSTVSTEKPCNTEEF 1364
                                                                                                                                                                                                      KITATTTQVTSTTTQDTT-----PFKITT---LKTTTLAPKVTTTKKTITTTEIM 955
                                                                                                                                                                                                                                                                                                                                                                                                                                          KKP-----APKE---LAPT--TTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPA
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	RESUL	E C	,											
		Q9SPM0		PRELIMINARY	NARY;	PR	'RT; 13	15 AA	•					
		01-MAY	-2000	(Trembi	rel. 1	`								
	ᄗ	01-MA3	1-2000	(Trembi	rel. 13. rel. 17	3, Last 7, Last		sequence up annotation	update) update	e)				
	GN	EXTENS	EXTENSIN-LIKE PROTEIN. PEX2.	E PROTE	N.									
	SS S	Zea ma	ıys (Ma	ize).	) )	) ; ;		•			,	,		
	88	Sperma	rota; v Lophyt	iridipı ə: Maqn	antae;	Strepto yta; Lil	ophyta liopsi	da``	Embryophyt; Poales;	a; Poa	Tracheophy ceae; PACC	cta	; lade;	
•	389	Panico	ideae;	Androp	ogonea	e; Zea.			, 1				9	
	RN X	ITT NCBL_	ax1D=4	5//;										
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		Hohors	ord s.	, вагие Зао М.,	Showa	alter A., I	, Bedi	Bedinger P.A.	P.A.;	., McCo	rmic			
		"Polle	n Exte	nsin-li	ke (Pe	x) Gene	s in a	Mono	ct	Di	cot."	~-		
		SUBMIT	AF1592	97; AAC	) TO T	ле <u>Емы</u> г	EMBL/GenBank/DDBJ	ומא/טטו	su databa	abases				
		Inter	ro; IP	R001611	; LRR.									
		Inter	TO; IP	R002965	P ri	ch exte	nsn.							
		Inter	ro; IP	R003592	; LRR_	out.								
		Pfam;	PF0056	0; LRR; 217; PR	3.	ENSN								
		PROSIT	E; PSO	0172; x	YLOSE_	ISOMERA	1;	UNKNOWN	Ň_1.					
		SEQUEN	SMART; SM003/0; LRR; 3. SEQUENCE 1315 AA; 134401 MW; 64	315 AA;	1344	01 MW;	64C97	A2A01F09	90936F	CRC64	٠.			
	Que Bes Mat	ery Mat est Loca etches	ろしび	h Similarity 55; Conserv	11.5 24.4 ative	%; Score %; Pred. 101; Mis	re 839 d. No. Mismat	839.5; I No. 1.5e smatches	DB 10; ;-47; 491;	Leng Indel	th 13 s 22	15; 17; Ga	Sq	ω 4-
	Qy	73 R	FESFE	RGRECDC	DAQCKK	RECDCDAQCKKYDKCCPDYESFCAEVHNPTS	YESFCA	EVHNP	PPSS	K-KAPPPS	PSGASQT	QTIKS	131	
	Db	390 €	QCAPVLA	APVLARPVEVDC	S	 	-KHVCA	KHVCAGYPTPGGPPSS	GPPSS	SVPGKE	VPGKPPSVPG	K	432	
	Qy	132 1	TTKRSPKPPNKKKTKKVIES	PPNKKKT	KKVIES	EEITEVK	ITEVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDF	TKKKP	PKPPV	VDEAGS	GLDNG	DFKVT	191	
	Db	433 -	1	LHGLGWG	PPDVSP	PAAPAPMPTPHTPPDVSPEPLPEPSPVPAPAPMRMPTLRSPPADE	PVPAPA	PMRMP	rLRSPP,	ADE	:	YIP	480	
	Qy	192 T	PDTSTT	DHNKVST	SPKITT	PDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNK	PSLPPN	ISDTSKI	TSLTV	NKETTV	ETKET	TTTNK	251	
	DЬ	481 T	PPVPA-	-KSPPGI	KSPPGTSPPASRGAP-	GAPPL	PLQAQPPAASSPPATTPV	ASSPP	ATPV		!	1	518	
	Qy	252 Q	H	STDGKEKTTSAKETQSI	ETQSIE	EKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKE	APTSKV	LAKPTI	KAETT	TKGPAL	TTPKE	PTPTT	311	
	Дb	519 -	 	KSSPF	PAAVVL	KSSPPPAAVVLPPPAKTPS	SPPAPV	-ASPPI	EAPVS	SPQPQVKSPPPI	KSPPP	PAPVA	568	
	QΥ	312 P	KEPAST	PKEPTP	TTIKSA	KEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTP	APTTTK	SAPTTI	-KEPAP	P	TTT	TTTKEPAP	363	
	Db	569 S	PPPPMKSP	ÞÞ	PARVASPPPLMKS	PPLMKSP	PPPPAPV	'ASPPQI	PPAPVASPPQPLKSPPPPVLWLSTPSVKS	PPVLWI	STPSV	KSPPP	626	
	Qy	364 T	TTPKEPA	PTTTKEP	APTTTK	SAPTTPK	!	-PAP TT	- ;	-KKPAPTTPKEPAPTT	TPKEP.	APTTP	413	
	В	627 F	PVPVASP	PPVKSP	PPLAPV	VASPPPPVKSPPPLAPVSSPSPPVKLP	2	APGKSTPP	PΕ	EKPTPP	TPVKS	SpppE	686	
	Qγ	414 K	KE-PTPT	[PKEPAP	TTKEPA		APTAPK	KPAPTI	[PKEPA]	KEPAPTTPKEPAPTTKEP	PAPTT	TKEPS	472	
	Db	687 K	TS	PTLTTSPPP	PPQEKPTPPSI	PSTPSKPP	PPPSPV	PPSPVETLPPP	SKSSPPEE	PEEPVS	PVSSPPQAP	PKSSS	746	
	Qy	473 F	PTTPKEPA	APTTTKS	APTTTK	PTTTKSAPTTTKEPAPTTTKS	KSAPTT	SAPTTPKEPSE	PTTTKEPAPTTPKEPAPTT	PAPTTP	KEPAP	TTPKK	532	
	Db	747 P	PA	PVSS	PPPLKS	SPPPVPES	SSPPPT	PKSSPP	LAPVS	SPPQVE	KTSPP	PAPVS	799	
	Qy	533 P	APTTP	KEPAPTTP	PKEPAPT	TTKKPAP	TAPKE	PAPTTP	KETAPTT	PKKLT	PTTPE	KLAPT	592	
	В	800 s	PPPTPKS	VAWTAdSS	SS	PPOVEKTSPP	PPPAPVSS	SPPPTPKS	(SSPPLA	4SSAd	POVEKT	rsppp	859	

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COSMID F35A5.
                                                                                                                                  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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8 (TrEMBLrel.
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Best Local
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STRAIN-BRISTOL N2;
Waterston R.;
Submitted (APR.1997) to the EMBL/CEMBL; U46675; AAB52641.1; -.
SEQUENCE 1274 AA; 138065 MW; (
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                                                                                                                                            TAPTTPKKLTPTTP----EKLAPTTPEKPAPTTPEELAPTTPEEP-----TPTTPEEPA
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Pred. No. 2.8e-47;
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                                                                                                                                                                                                                                                                                                                  Query Match 11.3%; Score 830; DB 10; Best Local Similarity 29.0%; Pred. No. 7e-47; Matches 321; Conservative 62; Mismatches 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LIE8 PRELIMINARY; PRT; 1480 AA.
Q9LIE8;
Q9LIE8;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL MALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; APO01306; BAB03062.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1480 AA; 147153 MW; D1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of & Sequence features of the TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Kato T.,
Submitted (MAR-2000)
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EMBL/GenBank/DDBJ databases
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                            VFMPEVTPDMDYLPRVPNQGIIINPMLS
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 VAIPPITKPPVATPPVTNPPTAMPPIVT
                                                                VATPPIAKPPTVLPPIAKPPVETSPTATPPTATPPVAIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIPPIATPPVAKPPVAT---PPTATPPIATPPIATPPVATPPTATPPVATPPIAKPPTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPKELAPTITKEPTSTTSDKPAPTTPKGTAP-TTPKEPAPTTPKEPAPTTPKGTAPTTL 743
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                                                                                               --TSRIAE
                                                                                                                                                              ATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP-----
                                                                                                                                                                                                                 ATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKT----ITTTEIMNKPEETAKPKDR
                                                                                                                                                                                                                                                              SKPPVATPPAATPPITTPPPAKPPVATPPIATPP--IAKPPVATPPTATPPIATSPVAKP
                                                                                                                                                                                                                                                                                  PGVPTTKTPAATKPEMT-TTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKIT
                                                                                                                                                                                                                                                                                                                                               PTTP-----ETPPPTTSEVSTPTTTKEPTTIH--KSPDESTPELSAEPTPKALENSPKE
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                                                                                                                               ATSPVATPPIAKPPTTTP--PTAT-PPVAMPPIATP---PTAKPPVATPPIANPPVEKPP
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                                                                                            -----AMLQTTTRPNQTPNSKL--VEVNPKSEDAGGAEGETPHMLLRPH 1069
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Best Local Similarity
Matches 313; Conserv
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EMBL; U48364; AAB18732.1; -.
EMBL; U48363; AAB18732.1; -.
MGD; MGI:106095; Naca.
InterPro; IPR002715; NAC.
InterPro; IPR003077; TS-N.
Pfam; PF01849; NAC; 1.
Pfam; PF01849; NAC; 1.
Pfam; PF0294; TS-N. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96312450; PubMed-8698236;
Yotov W.V., St-Arnaud R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK-----VSTSPKIT
                                                                                   GVPVTLTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP-----SPQKIPKVAGPKEAS
                                                                                                                                                                                                                                                                                        APTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKE
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                            ATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTA
                                              ISPSPKKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPASK
                                                                                                                                                                        PSPTTTKEPAPTTPKEPAPTTPKKPAPTT - - PKE - - - - - - -
                                                                                                                                                                                                    IPSAPQKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGE
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                                                                                                              -TTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELA
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smatches 436;
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                                                                                                                   Matches
                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                   STRAIN-B73; TISSUE-POLLEN;
Rubinstein A.L., Broadwater A.H., Lowrey K., Bed
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ da
EMBL; Z34465; CAA84230.1; -.
Mendel; 14346; Zeama; Z368; 14346.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR.out.
Pfam; PF00566; LRR; 3.
SMART; SM00370; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q41805;
Q41805;
                                                                                                                                                                                          SIĞNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (Maize).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTENSIN-LIKE PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                     Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 TPNSKLVEVNPKSEDAGGAEGETP
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                                                                                  RECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAAPQTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-PVTT--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVPPVKNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSI
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                          KKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ
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                                                           RPVDCS
                                                                                                                   246;
                                                                                                                                 Similarity
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VSPEPLPEPSPVPAPAPMPMPTPHSPPAD-----
                                                                                                                   Conservative
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120980 /
                                                                                                                                 10.9%;
                                                        KHVCAGYPTPGGGPPSSPVPGKPAASAPMPS----PHTPPD
                                                                                                                 64;
                                                                                                                                                                                       POTENTIAL.
MW; 2C77C7F8D7130149
                                                                                                                Score 800; DB 10;
Pred. No. 5.4e-45;
4; Mismatches 401
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                                                                                                                   401;
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J databases
                                                                                                                                             Length 1188;
-DYVPPTPPVPGKSPP
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01-MAY-2000 (Tr)
01-MAY-2000 (Tr)
01-JUN-2001 (Tr)
CG4090 PROTEIN.
CG4090.
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goc. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A.,
                                                                                                 SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPKPASPPAHVSSPPEVVKPSTP--PAPTTVISP-PSEPKSSPPPTPVSLPPPIVKSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPPLAPVSSPPQVEKTSPPPAPLSSPPLAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTPVSSPPALAPVSSPPSVKSSP----PPAPLSSPPPAPQVKSSPPPVQVSSP-PPAPKS
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SMART; SM00494; ChtBD2; 11.
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InterPro; IPR000561; EGF-like.
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   RCVDNDRGGFNMVPFSCGPGTVWDAQMQACNHAWAVKECGGIAPPTTSTPTTSR-PTTAS
                                                                                                                                          NQSTSSSTSSSSSNNNNQGSSSSSSSSSSSTSSKPNPSETCKVNGQFIGDRSDCAKFY 1175
                                                                                                                                                                                                               KEKTTSAKETQSI-----EKTSAKDLAPTSKVLAKPTPKAETTTKGP------
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A; 219547 MW;
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Pred. No. 6.5e-42;
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Baldwin D.,
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PKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTKEPAPTTPKEPAPTT-----

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-PTTARPVTARPTTSSPTTASSSQTTSPVTQAPNTDGKCRS 1290

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                                                                                                                                                                                                                                                                                                       Q9XDH2 PRELIMINARY;
Q9XDH2;
Q1-NOV-1999 (TrEMBLrel. 12, C
Q1-NOV-1999 (TrEMBLrel. 12, L
Q1-JUN-2001 (TrEMBLrel. 17, L
PROLINE-RICH MUCIN HOMOLOG.
Espitia C., Laclette J.L., Mondragon-Palomino Zhang Y., Moreno C., Singh M.; "Cloning and characterization of a new member is a useful marker of polymorphism in Mycobact
                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID-1773;
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                                                                                                                  STRAIN-H37RV;
                                                                                                                                         SEQUENCE FROM N.A.
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Best Local Similarity 28.2%;
Matches 248; Conservative 3
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PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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TSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGET
                                                SMALPPAPPDPPIPLLATPPAPPAPPLPMSPPAPPLPPAAPDPPAPPLTINQPPSPPLAP
                                                                                                                PAAPPAPPAPPVRATTP
                                                                                                                                           TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN
                                                                                                                                                                                                        KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI
                                                                                                                                                                                                                                                            KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSAEPTPKA--LENSP
                                                                                                                                                                                                                                                                                                        APPAPSMPSAVRVPPSPPIPPAPPAAPRASMPALPPAPPSPPATRLCPPLPPSPPAPNSP
                                                                                                                                                                                                                                                                                                                                   KEPAPTTP---KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET---APTTPKEPAPTTP
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                                                                              SKATTPKPQKP----TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTM-----PELNP
                                                                                                                                                                            --PAPPAPPAPPSALPFVNPPA-------PPTPAAPK--
                                                                                                                                                                                                                                        --PAPPAPPTPPKLLS--ANPPCPPVPPAPNRPPAPPAPPAPPELPAPPDPPTPPVANSP
                                                                                                                                                                                                                                                                                                                                                                    --PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP
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9; Mismatches 361;
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Db 726 VPGAPLAPLPINGRPVFARKNSLI------GSSSGDT 756
Search completed: April 26, 2002, 16:30:16
Job time: 631 sec

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Result
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Q9n45 caenorhabdi
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Q9i751 drosophila
Q96449 phytophthor
Q9spm0 zea mays (m
Q2007 caenorhabdi
Q91168 arabidopsis
Q41805 zea mays (m
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## ALIGNMENTS

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A TUTNER K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Lea Tutner K.J., Fitz Grandti J., Calvetti J., FitzGerald M., Kriz R. Kelleher K., Giannotti J., Eraser H., Bean K., Norton C.R., Ges Ferenz C., Grobholz J., Eraser H., Bean K., Norton C.R., Ges Bhatia S., Kriz R., Hewick R., Clark S.C.;

A Bhatia S., Kriz R., Hewick R., Clark S.C.;

A Bhatia S., Kriz R., Hewick R., Clark S.C.;

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A Bhatia S., Kriz R., Hewick R., Clark S.C.;

A Bhatia S., Kriz R., Hewick R., Clark S.C.;

A Bhatia S., Kriz R., Hewick R., Clark S.C.;

B InterPro; IPR000585; Hemopexin.

B InterPro; IPR001512; Somatomedin_B.

R InterPro; IPR002400; GF_Cysknot.

R Pfam; PF00045; hemopexin; 2.

R Pfam; PF01033; Somatomedin_B; 2.
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Merberg D.M., Fitz L.J., Temple P., Giannotti J.

FitzGerald M., Scaltreto J., Kelleher K., Preiss
Jacobs K., Turner K.;

(In) Preissner K.T., Rosenblatt S., Kost C., Weg
Mosher D.F. (eds.);
Biology of vitronectins and their receptors., pp.
Elsevier Science Publishers B.V. (1993).
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Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Rulleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.;

Blacod 78:279-279(1991).
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEGAKARYOCYTE STIMULATING FACTOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SEQUENCE 1404 AA; 151090 MW; AABD7A
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                   KPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPT 725
                                                            TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK 665
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Pred. No. 0;
O; Mismatches
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180	TECT CONTINUES OF THE PROPERTY	j
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120	61 KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP	Dβ
24	25	Qy
24	1 MAWKTLPIYLLLLLSVFVIQQVSS	Оy
iaps 1	ry Match 98.3%; Score 6455.5; DB 4; Length 1404; t Local Similarity 87.3%; Pred. No. 0; ches 1226; Conservative 0; Mismatches 3; Indels 175; G	Que Bes Mat
	SEQUENCE FROM N.A.  Wray P.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. Submit, AL13353; CAC36090.1; EMBL; AL133553; CAC36090.1; EMBL; AL133553; CAC36090.1; SEQUENCE 1404 AA; 151076 MW; 782A11746B3FDEE5 CRC64;	RA RE
	Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;	
	01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR ). BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR ).	
	LT 2 49 Q9BX49 PRELIMINARY; PRT; 1404 AA. O9BX49;	838
	1206 PSRTARAITTRSGQTLSKVWYNOP 1229 	Qу
1205 1380	1146 SPARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1 	Qy Db
32	CPGRRPALNYPYYGEMTQVRRRRFERAIGPSQTH: 	Qу
26	1026 RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY 1 	Qy Db
1025	966 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT 1	Оy
965 1140	906 QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS 9 	Qy Db
0 0	846 POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN 9 	Qy Db
845 1020	786 TSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPK 8 	Оy
960	901 TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTOV 9	рь

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FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSQTHTIRIQY
                                RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                                            DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFT
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	PS00524; SOMATOMEDIN_B; 2. 1054 AA; 115991 MW; 4FC64BFA42283235 CRC64;	PROSITI SEQUENO	SQ DR
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	R00022; SOMATOMEDINB.	PRINTS SMART;	DR DR
	R01217; PRICHEXTENSN.	Ptam;   PRINTS	DR DR
	<pre>IPR002965; P_rich_extensn. IPR001212; Somatomedin_B.</pre>	InterP	DR DR
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	ARAITTRSGQTLSKVWYNCP 1404	1381 P	Db
	SRTARAITTRSGQTLSKVWYNCP 1229	1206 P	Qy
	SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1380	1321 SI	Db
	YODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAF	1146 SI	Qy
	FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGETTQVRRRRFERAIGPSQTHTIRIQY 1320	1261 FI	DЬ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKAT-----TPKP-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPK
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                                                                                                                                                                                                                                                                                                                                                                             PMRVSYQDKGFLHNEVKVSTMWRGFPNVVTSAITLPNIRKPDGYDYYAFSKDQYYNIDVP
                                                                                                                                                                                                                                                                                                                                                                                                       PARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPTKAPKKPTSTKKPKT-PKTRKPKTTPAPLKTTSATPELNTTP---LEVMLPTTTIPKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TTLKATTLAPKVTAPAE-----EIQNKPEETTPASEDSDDSKTTLKPQKPTKAPKPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TPKEPEPTTPKEPEPTTPKEPEPTTP-------KEPEPTTPKKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRGGNIQQYTYKQEPMKKCTGRRPAINYSVYGEAAQVRRRRFERAVGPFQTHTFRIHYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCEGKTFFFKDSQYWRFTNDVVDPGYPKQIVKGFGGLTGKIVAALSIAKYKDRPESVYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNPETAEVNPDHEDADGGEGEKP-LIPGPPVLFPTAIPGTDLLAGRLNRGININPMPSDE
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  (Bovine)
                    (TIEMBLrel. 08, Created)
(TIEMBLrel. 08, Last sequence up
(TIEMBLrel. 17, Last annotation
ZONE PROTEIN (FRAGMENT).
                                                                                                                                                    PRELIMINARY;
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Best Local :
                                                                                                                     O9N4S7; PRELIMINARY;
O9N4S7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00120; HX; 2
NON_TER 1
SEQUENCE 401 AA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. MCBI_TaxID=9913;
                                                                  Eukaryota; Metazoa; Rhabditidae; Pelode
                                                                                                                                                                                                                                             1191
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                                                                                                                                                                                                                                                                                                                                                                           1011
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           STRAIN-BRISTOL N2;
MEDLINE-99069613;
                                 SEQUENCE FROM N.A
                                                     NCBI_TaxID=6239;
                                                                                      Caenorhabditis elegans
                                                                                                 Y51B11A.1 PROTEIN
Y51B11A.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000585; Hemopexin.
Pfam; PF00045; hemopexin; 2.
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                                                                                                                                                                                                                                                                                                                                                       183
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                                                                                                                                                                                                                                                                                                                                                                  TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA 1070
                                                                                                                                                                                                                                                                                                                                                                                                          PRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRI
                                                                                                                                                                                                                                                                                                                                                      TEVWGIPSPIDTVFTRCNCEGKTFFFKGSQYWRFTNDIKDAGYPKLISKGFGGLNGKIVA
                                                                                                                                                                                                                                                                                                                                                                                               VRGPSQGFGINPMFSDETNLCNGRPVDGLTTLRNGTLVAFRGHYFWMLTPFTPPPPPRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LPEAMLQTTTRPTPTPNSEIIDVNSENEDGDAAEGEKPHMIFRPPVLTPIVIPGTEII 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKGRATNSQVTTPKPQKPTKAPKKPTSTKKPRT-PRVRKPKTTPTPPKTTTSAMPEPTPT
                                                                                                                                                                                                                                                                                                            ALSIAQYKSRPESVYFFKRGGSVQQYTYKQEPTQKCTGRRPAINYSVYGETAQVRRRRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                  Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0:0-0(1998).
AAD13404.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein, Synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes
              PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44952 MW;
                                                                            Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.1%;
80.2%;
                                                                                                                       15,
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17,
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                                                                  Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                        Last sequence up
                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1713.5; DB 6
Pred. No. 2.8e-107;
                                                                            Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuettner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86147CC9AFBB73D7 CRC64;
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by Cells Lining Synovial
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                                                                                                                                                                    ΑA
                                                                                                                                 update)
                                                                              Rhabditida;
                                                                                                                        update)
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                                                                              Rhabditoidea,
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Query Match 14.8%; So
Best Local Similarity 29.9%; Pr
Matches 327; Conservative 137;
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Submitted (MAR-2000) to the EMBL/Gen.
EMBL; AC006797; AAF60743.1; -.
InterPro; IPR002965; P.rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of C. elegans cosmid Y51B11A."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
      720
                                 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                 APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPK
                                                                                  TTPVQTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPET
                                                                                                     TTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKP-APTTPKETAPTTPKEP
                                                                                                                                                                                                                                                                               KEP--APTTPKETAPTTPKKLTPTTPEKLAPTTPEEKPAPTTPEELAPTTPEEP--TPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKSPAPTTTKSA
EPGVPTT - - KTPAATKPEMTTTAKDKTTERDLRTT - - - - PETTTAAPKMTKETATTTEKT
                                                                                                                                           ETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPE---TTSTEPPSSS
                                                                                                                                                            EPAPTTPKKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTTPKEPAPTTPKEP--AP
                                                                                                                                                                                                    VQTTTTT----APETTSTESPSSSTTPVQTTTTTAP
                                                                                                                                                                                                                      TEPPSSSTTPVQTTTTTAPETTSTEP----PSSSTTPVQTTTTTAPETTSTEPPSSSTTP
                                                                                                                                                                                                                                                                                                                    ----TTPVQTTTTT----APETTRTEPPSSSTTPVQNTTTTAPETTSTEPPSSSTTPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       PETTSTEPPSSSTTPVQTTTITAPETTSTEP-PSSSTTPVQTTTTTAPETTSTEPPSSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTAPETTSTEPPSSSTSPVQTTTTAPETTSTEAPSSSTTPVQTT-----TTTAPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSTPTSSSTPIKETTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEAPSSSTTPVQT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 969; DB 5;
Pred. No. 6.3e-57;
87; Mismatches 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472; Indels 156;
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 773
                                                        719
                                                                                    681
                                                                                                                                                                                                                                 543
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kul nt s son	P. E. Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei H. McIntosh T. C. Moreod M. B. McDerzon Din X.,	HAITIS N.L., HAIVEY D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei MH., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison T.A., Korchum K.A.	C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischma	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	Proketain D., Bo	h C., Baldwin D., ., Beasley E.M.,	Helt G., Nelson C.R., Miklos G.L.	Chen L.X.,	., Galle R	ocayne	STRAIN=BERKELEY;	SEQUENCE FROM N.A.	27;	ptera; Brachycera; Mus	lanogaster (Fruit fly). tazoa; Arthropoda; Tracheata; Hexapoda	228.	7, Last annotation upda	MAR-2001 (TrEMBLrel. 16, Created)	7S1;	6	1060WSYNN 1064	1035 FFKDSQYWRFTN 1046	SIDLPFYNVPTGLE-IWPEINCEGNK- 1	VAFRGHYFWMLSPFSPPSPARRITEVWGII	962 YIDRVVYPETTEWWENKRDIIIQSYDSPRRTAFSFVSTEDIGTCTAILTCIYTSEGGISN 1021	INPMLSDETNICNGKPVDG	908 APETTSTEPPSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTVPCDCSLS 961	SEDAGGAEG-ETPHMLLRPHV	848 PSSSTSPVQTTTTTAPETTSTEPPSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTT 907	TPRK	792 TAPETTSTEPPSSSTSPVQTTTTAPETTSTEPPSSSNTPVQTTTTTAPETTSTEP 847	FKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETA-KP 6	732 PPSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSNTPVQTTTT 791

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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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Science 287:2185-2195(2000).

EMBL; AB003495; ABG22353.1;

FlyPase; FBgn0030561; CG5228.

SEQUENCE 1049 AA; 107278 MW; 954DD629E7619671 CRC64;
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Shue B.C., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKPTTLKPTEGTSAKPTTLKPTEGTSAKPTTLK--PTEGTTAKPTTLK--PTEGTSAKPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGKEKTTSAKET--QSIEKTSAK--DLAPTSKVLAKPT-----PKAETTTKGPALTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KITTAKP-----INPRPSLPPNSDTSKETSL----TVNKETTVETKETTTINKQT--ST
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                                                                            TKGPTSTTSDKPAPTTPKE--TAPTTPKEPAPTTPKKPA---PTTPETPPPTTSEVSTPT
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                                            TLNPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGT
                                                                                                                                  PTTLKPTEGTTAK---PTTLK---PTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTAKPT
                                                                                                                                                                              PTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK----
                                                                                                                                                                                                                                                                                                              PTTLKPTKGTTAKPTTLK----PTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLK
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Pred. No. 5.8e-55;
6; Mismatches 443;
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RA Addams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andams M.D. (Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Berson R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Burton G.G., G.L.G., Ra Ballew R.M., Baswendale J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Baroktatin D., Botshakov S., Borkova D., Botchan M.R., Bukler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Gepabor K., Cawley S., Dohnes M., Dugan-Rocha S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Goog F., Gorrell J.H., Gu Z., Guan p., Harris M., Glasser K., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McEod M.P., Lai Z., Liang Y., Lin X., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Ra McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Liang Y., Lin X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Ra McHall M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Ra McHall M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Welson D.L., Reese M.G., Ra Shue B.C., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Shue B.C., Siden K
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01-NOV-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
EG:56G7.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETAKPKDRATNSKATTPKPQKPTKAPK---KPT--STKKPKTMPRVRKPKTTPT---PRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKK--TITTTEIMNKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQPTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTSAQPTTLKPTERTSAQ--PTTLKPTEGTTAKPTTLKPTKGTSGQANNFETKRKERRP 1045
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Metazoa; Arthropoda; Tracheata; H
Neoptera; Endopterygota; Diptera;
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; Tracheata; Hexapoda; Insecta;
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Baldwin D.,
               H.O.,
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Best Local Similarity
Matches 276; Conserv
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                                                      PTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP-TTTKGPTSTTSDK
                                                                                                          PKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPT--STTSDKPAPTTPKGTA
                                                                                                                                                                  PAPTITKKPAPTAPKEPAPTTPK-ETAPTTPKKLTPTTPEKLAPTTPEKP-----AP
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genome sequence of Drosophila melanogaster.";
nce 287:2185-2195(2000).
                                                                                            PLTTLSTEEPNTTPKPLRTTTPTTTSVTATTRITTTTISESSTETTSTQKPKSTTPTSTT
                                                                                                                                               TSSTORATSTTSEPTKTT-ONITTTPKPTTLKTSTOEATTSTOKVSTVTITTKKATESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 865.5; DB 5; 28.5%; Pred. No. 9.3e-50;
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Best Local Similarity
Matches 355; Conserv
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SEQUENCE
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYST GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRECURSOR.
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STRAIN-RACE 1-11;
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; Pred. No. 5.3e-49;
46; Mismatches 475;
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 Stratford S., Barnes W., Golubiewski A., Cotter R., McCormick Hohorst D., Gao M., Showalter A., Bedinger P.A.; "Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.";
                                                                                         Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Panicoideae; Andropogoneae; Zea.
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                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT-TTKSAPT--TPKEPSPTTTKEP-----APTTPKEPAPTTPKKPAPTTPKEPAPT--
                                                                                                                                                                                                                                                                                                                      QTPNSKLVEVNPKSEDAG
                                                                                                                                                                                                                                                                                                                                                                                                    TTLAPKVTTTKKTITTEIMNKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYAP----TEETTYEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEPTPKA-LENSPKEPG-----VPTTKTPAATKPEMTTTAKDKTTERDLRTTP----ETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAPAEETPYEPTEETTYAPTEETTYAPTEETMYAPIEETTYGPTEETTY-APTEATTYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAPTEETPYEPTEETTYAPTKETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEE
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                                                                                                                                                                                                                                                                                             QGINGIGVENKVRYNNAG
                                                                                                                                                                                                                                                                                                                                                  PAEESTSTVSTEKPCNTEEFTDEPTDEPTDE--PSDEPTDEPTDEPTDLPTDEPSTPCDN
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                                                                                                                                                              PROTEIN.
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Last sequence update)
Last annotation update)
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                                                                                                         Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC clade;
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R InterPro; IPR001611; LRR.
R InterPro; IPR001998; XyLose_isom.
InterPro; IPR002965; P_rich_extensn.
R InterPro; IPR003592; LRR.out.
R Pfam; PF00560; LRR; 3.
R PRINTS; PR01217; PRICHEXTENSN.
R PR.NTS; PR01217; PRICHEXTENSN.
R PR.NTS; PS001772; XYLOSE_ISOMERASE_1; UNKNOWN_1.
R SMART; SM00370; LRR; 3.
SMART; SM00370; LRR; 3.
SMART; SM00370; LRR; 3.
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Best Local Similarity
Matches 255; Conserv
1147
                                                             1097
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 SPPP--
                                                                                PETPPPTTSEVSTPTTIKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA
                                                                                                                                                                                                                  KPAPT---
                                                                                                                                                                                                                                                                            TTPKETAPTTPKGTA------PTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD
                                                                                                                                                                                                                                                                                                                                      KPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                  TTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PAPVS--SPPPLKSSPPPVPESSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPTLTTSPPPQEKPTPPSTPSKPPPPSPVETLPPPSKSSPPEEPVSSPPQAPKSSSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASPPPPVKSPPPLAPVSSPSPPVKLPPLPAPGKSTPPPEEEKPTPPTPVKSSPPPEKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTP-KEPAP-----TTTKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPPATPVKSSPPPAAVVLPPPAKTPSPPAPVASPPPEAPVSSPQPQVKSPPPPAPVASPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIEKTSAKDLAPTSKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPVPAPAPMRMPTLRSPPADEYIPT----PPVPAKSPPGTSPPASRGAPPLQAQPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSLPP-----NSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTP-----KPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPR
                              TKPEMTTTAKDKTTERDLRTTP----
                                                           VSSPPPAPKSLPPPTPVSSP
                                                                                                                                                      TPKKPAPKELAPTTTKGPTSTTSDKPAPTT--PKETAPTTPK----EPAPTTPKKPAPTT
                                                                                                                                                                                                                                               LAPISSPPSEPKSPSSPPMVEKTSPPPATVSSPPPTPKSSPPP---APVSSPPPVVKSSP
                                                                                                                                                                                                                                                                                                         SSPPLEPKPSSPPSSVSSPPTTVKSSPPPAPLSSPPMTPKSSSPPAHVSSPPEAEKSSPP
                                                                                                                                                                                                                                                                                                                                                                     PTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPV
                                                                                                                                                                                   PPAPVSSPPPTPKPLPPPAPVSSPPPVVKSSPPPTPVSSPPPTPKPLPPPPTPVSSPPPT
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                                                                                                                                                                                                                -TPKGTAPTTP--
                                                                                                                         APVSSPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%;
 -ELKSSPPPAPVSSPPSAPKSSPPPAPVSLPPPEVKSSPPPAPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 808.5; DB 10;
Pred. No. 4.4e-46;
B8; Mismatches 459;
                              ETTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                        -KEPAPTTPKEPAPTTPK--GTAPTTLKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808.5; DB 1
No. 4.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KPAAPAPMPTPHTPPDVSP----EPL-PE
                                                             PPEVKSSPPPTPVSSPPPAPKSSPPPTPVS
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                                                                                                Query Match
Best Local Sim
Matches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;

MEDLINE-94150718; PubMed-7906398;

Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Alnscough R., Connell M., Copsey T., Cooper J., Coulson A

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Latreille P.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Ropera A., Saunders D., Shownkeen I

Smaldon N., Smith A., Soonhammer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                Waterston R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U46675; AAB52641.1; -.
SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C1799F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 01, 01-NOV-1998 (TrEMBLrel 08, COSMID F35A5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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STRAIN-BRISTOL N2;
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                                              KNRTKK-KP-----TP-----KPPVVDEAGSGLDNGD----FKVTTPDTSTTQHNKVSTS
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Pred. No. 1.2e-45;
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ADFTMPAPKKPDTEDP
                                                                                     IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK----
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                                                                                                                                                                                                                                                                                                                                                                                                                 KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT-----TPKKPAP-----KEL
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                              ---TTPTPRKMTSTMP
                                                               -LNKKAPAEKPTEK-----
                                                                                                                              KWKPVWDDDPDEPEADFTVPAPSKKPDTEDPADPLG---
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RESULT 11 Q9LIE8 ID Q9LIE8

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STRAIN=COLUMBIA;
Kaneko T., Kato T., S
Submitted (MAR-2000)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:217-221(2000).
EMBL; AP001306; BAB03062.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1480 AA; 147153 MW; D1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of A
Sequence features of the
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=COLUMBIA;
PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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622
                             509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTS----PKITTAKPINPRPSL 89
                                                                                                                                                   TPKEPAPTTPKEP--APTTTKKPAPTAP--KEPAPTTPKETAPTT-----PKKLTP--T
                                                                                                                                                                                                         TITKSAPTTIKEPAPTITKSAPTIPKEP--SPTITKEPAPTITKEPAPT 404
                                                                                                                                                                                                                                                                                                                                                                                 PVAAPPITNPPISKPPVTTP----PTTTPPIAKPPIATPPISTPPAATPPAATPPITTLP 326
TPPIATPPIAKPPVATPPTATPPIATSPVAKPPVATPPIKTPPPAKPPVAIPPIATPPVA 681
                            TPKEPAPTTPKEPAPTTPKETAP - - TTPKGTAPTT - - - LKEPAPTTPKKPAPKELAPTTT
                                                           TPPTATPPVAKPPVATPPIATPPTAKPPISTPPISKSPVATPPAATPPITTPPPAKPPVA
                                                                                         TPEKLAPTTPEKPAPTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNT---PKEPAPT
                                                                                                                        TPPLAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVATPPIAKPPVVTPPTT
                                                                                                                                                                                         TAT--
                                                                                                                                                                                                                                                    VATPPTATSPIKTPPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPP
                                                                                                                                                                                                                                                                                    TTKEPAPTTP-KEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTT----KEPSPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                KEPAPTTT-----KSAPTTPKEPAPTTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              TQMPPIATP-PIAKSPVATPPIATPPTATPPITIPPVATPPITTPPIANPPIIMPPIATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKV--LAKPTPKAETTTKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPPPSTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPRPHPKPPNVK-----PHPHPKPPTKPHPHPKPPTKHHPHPKPPTIKPPPKPPSV
                                                                                                                                                                                                                                                                                                                   PAKPPVAISPIVT--PPVTPIAQPPVATPPTATPPVATPPIATPPTSKSPISTPPISESP
                                                                                                                                                                                                                                                                                                                                               PA-----PTTTKSAPTTP-KEPAPTTPKKPAP--TTPKEPAPTTPKEPTPTTPKEPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 29.0
07; Conservative
                                                                                                                                                                                         -PPVAKPPVETPPIATPPTAKPPISTPPISKPPVATPPAATPPITTPTPVKPPVA
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29.6%;
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PPTTNPPPSTPQPPTHKPPPCTPTPPVASPPMATPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 800.5; DB 10; Pred. No. 1.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505;
                                                                                                                                                                                                                                                                                                                                                                                                             --KEPAPTTPKEPAPTTTKE
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	93 SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 152	Qy
	PHSPPADD	Дb
	37 PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPN 92	Qy
$\omega$	11.9%; Score 784; DB 10; Length 1188; est Local Similarity 29.9%; Pred. No. 1.7e-44; atches 230; Conservative 59; Mismatches 359; Indels 122; Gaps	Que Bes Mat
	SIĞNAL 1 27 POTENTIAL. SEQUENCE 1188 AA; 120980 MW; 2C77C7F8D7130149 CRC64;	SQ
	SMART; SM00370; LRR; 4.	DR KW
	Interpro; IPR001611; LRR. Interpro; IPR003592; LRR_out. Dfam. pe01560: LRR. 3	DR DR
	2MBL; Z34465; CAA84230.1; 4endel; 14346; Zeama;2368;14346.	DR DR
	STRAIN-B73; TISSUE-POLLEN; Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.; Submitted (JHN-1994) to the EMBL/GenBank/DDBJ databases.	R RA
	SEQUENCE FROM N.A.	RP
	Panicoideae; Andropogoneae; 2 NCBI_TaxID=4577;	1 × 8
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;	88
	EXTENSIN-LIKE PROTEIN Lea mays (Maize).	OS
	01-JUN-2001 (TrEMBErel. 17, Last annotation update)	DI
	)1-NOV-1996 (TrEMBLrel. 01, Created)	338
	0041805 PRELIMINARY; PRT; 1188 AA.	SUS
	ULT 12	RESU
	1071 ATPPUTNEPTAMEPIVT 1087	ф
	949 YLPRVPNQGIIINPMLS 965	Qy
	1026 VLPPIAKPPVETSPTATPPTATPPVAIPPVVKPPVAIPPITKPPV 1070	Db
	KSEDAGGAEGETPHMLLRPHVFMPE	Qy
	972 KPPTTTPPTAT-PPVAMPPIATPPTAKPPVATPPIANPPVEKPPVATPPIAKPPT 1025	Db
	TKAPKKPTSTKKPKTMPRVRKPKTT	Qy
	915 PAKPPVAIPPIATPPVAKPPVATPPTATPPIATSPIATPPVVTPPTATSPVATPPIA 971	Db
	KTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSK	Qy
	857 TPPITTPPPAKPPVATPPIATPPIAKPPVATPPTATPPIATSPVAKPPVAIPPIKTPP 914	Db
	RTTPETTTAAPKMTKETATTTEKT	Qy
	797 TPPIAKPPVATPPTTAPPTATPPVAKPPVATPPIATPPTAKPPILTPPISKPPVATPPAA 856	Db
	PPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKT	Qy
	737 MPPIATPPTAKPPIATPPIAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVA 796	Db
	-ĭ	Qy
	682 KPPVATPPTATPPIATPPIATPPVVTPPTATPPVATPPIAKPPTTIPPTATPPVA 736	Db
	TTSDKPAPTTPKGTAP-TTPKEPAPTTPKEPAPTTPKGTA	Qy

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                                      SEQUENCE FROM N.A.

MEDILINE-96312450; PubMed-8698236;

YOLOV W.V., St-Arnaud R.;

YOLOV W.V., St-Arnaud R.;

Totor W.V., St-Arna
                                                                                                                                                                                                                                                                                                                                                                                                                                           P70670 PRELIMINARY; PRT; 2187 AA.
P70670;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE (ALPHA-NAC.
                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                               NACA
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                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPPPAP----VKPPSLP-PPAPVSSPPPVVTPAPPKKEEQSLPPPAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSPPPPAPISSPPPPVKSPPPPAPVS--SPPPPVKSPPPPAPVSSPPPPIKSPPPPAPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA---PKSSPPPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL
  IPR002715; NAC. IPR003037; TS-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA----PTTPKK----PAPKELAPTTTKE---PTSTTSDKPAPTTPKGTAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                       FORM GP220).
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                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                             converts
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; Murinae; Mus
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Best Local S
Matches 292
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Pfam; PF02094; T
SEQUENCE 2187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISAVQSPKVDPIMSDVTPTSPKKTSA-----TAVPKDTSATLSLKSVPAVTSLSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEISPSPKKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEPAPTTTKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E---TPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPAPTTPKEPTTTKEPAPTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATSSSKRAPKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTTKEPAPTT -- TKSAPT ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKGPPATLAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTSKKAT---EIAASKDVSPSQ--FPKEVPLLQHV---PPTSPPKSPVSDTLSGALTSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAPVAPSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPSPQKTPKSVSLKGAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTAKPINPRPSLPPNSDTSKETSL--TVNKET-----TVETKETTTTNKQTSTDGKEK 128
                                                                                                                                                                                                                             SKKLSQTVGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SP
                                                                                                                                                                                                                                               KEPTS-----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAP
                                                                                                                                                                                                                                                                                        TAPVQIPPSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPS
                                                                                                                                                                                                                                                                                                                  TTPKETAPTTPKGTAPTTLKEPAPTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                       SKGVPVTLTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP-----SPQKIPKVAGPKE
                                                                                                               TPAVPPVKNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASP
                                                                                                                                                                       SSPKK-APKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPV
                                                                                                                                                                                             TTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP-
                                                                                                                                                                                                                                                                                                                                               ASATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEIPSAPQKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVS
SPATAAPQTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMS
                                                      SIK-PVTT--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASL
                                                                                TTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQ
                                                                                                                                         ----PPTTSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVP
                         VTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTP
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27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 778.5;
Pred. No. 7.8e
19; Mismatches
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RESULT
OPERATOR

AC Q9

DT Q9

DT Q9

AC Q9

DT Q1

CGG

GN CGG

GN CGG

GN CGG

CGG

RA AM

RA AM

RA AM

RA AM

RA BE

RA AM

RA BE

RA BE

RA BE

RA DU

RA BE

RA Ha

RA Me

RA Sp

RA Tin

DR FI

DR FR FI

DR FR FR

TR SC

SQ SE

SQ SE
                                                                              RX MEDILLE-20196005; PubMed-10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pefiffer B.D.,
RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pefiffer B.D.,
RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pefiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Hayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishkov S.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.V.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Borlow R.M., Doup L.E., Downes M., Dung P., Dowle, D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
ROSIEr C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Durbin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. L.,
RA Merkulov G., Jeit Y., Levitsky A.A., It J., Li Z., Liang Y., Lin X.,
RA Mount S.M., May M., Murphy B., Murphy L., Muzny D.M., Melson D.L.,
RA Mensen K.A., Bowland T.G., McLeed M.P., McCherson D.,
RA Merkulov G., Stabina N.V., Mobarry C., Morils J., Moshrefi A.,
RA Mensen K.A., Rowley S., Pollard J., Puri V., Reese M.G.,
RA Mensen K.A., Mowley S., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mensen K.A., Mowley S., Staben D., Skupski M.P., Smith T.,
RA Spier E., Staden K.A., Mixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M.P., Weltscock G.M., Weissenbach J.,
RA Hostin D., Weissenbach J.,
RA Hostin D., Weissenbach J.,
RA Hostin M.R., Shang S., Stabin M.P., Smith T.,
Ra Spier S., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
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    PROSITE; PS00022; SEQUENCE 2112 A/
                                                   SMART; SM00494; ChtBD2; 11.
                                                                       Pfam; PF01607; Chitin_bind_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
CG4090 PROTEIN.
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EGF_1; 1.
A; 219547 MW;
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Last sequence update)
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B91018E5551A5D36 CRC64;
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AKDKTTERDLRTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQD 792 ::     :			
ETTTAADKMTKETATTTEKTTESKTTATTTOVTSTTTOO 70		(Ji	дь :
TESTTSSGKPET1	SSD	1817	g g
TTTKEPTTIHKSPDESTPELSA	ETPPPTT	67	Qy
RYYRCVDAAKNGKYQVYAFKCGKGTVWDTSTETCNYADQVSGN 1816	GFFPDPEDCS	1764	Db
KPAPI	PAPKELA	622	80
TTTT-LPSTTTDAIQEPTTSKKPEPTTTTESPESSTPEGSVTTLQPEPQPNYNCSSE 1763	된 -	1705	В
-PAPTTPKGTAPTTLKEPA	- 日 - 日	565	Qy
TEYPOKPTTEEPTTTSIPGYNPTTTSVPGYNPTTTPIPVETTTSTPGYKPTTTG 1704	PTT	1648	Dр
\PTTPKGTAPTTLKEPAPTTPKKPAPKEL	PAP	513	Qy
PEKPQKPT-TTEYPQKPTTTEEPTPEKPQKPT-TTEYPQKPTTTEEPTPEKPQK 1647	TTEE	1592	Дb
TTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEP!	- H	453	Qy
EESKDPGSTTPQSTDEPTTVTKPI-TKPTE-EPSTEKPQKPTTQYPEKPT 1591	PAEPITTTPS	1534	Db
KEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT 452	PKKPAPTTP-	398	Qγ
CTGEGYMADPEDCRKYYRCINAGASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCSKL 1533	Ħ	1474	DЬ
EPAPTT 397	8	388	Qy
PTTTGLPPTTTTGAQPTTTTLSSETETSTVTTSPESTTQPPSTTTMKPLPAG 1473	TTTTSLP	1414	Дb
PKE	PTTTKEPSPT	333	Qy
PPTTTDLPPTSTTGLP-PTTTBLPPTTTTDLPPTTTTRLPP 1413	4 TSTSSTTTP-	136	DЪ
EPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPA 332	3 PKEPAPTTE	27	Qy
SIPFQCGAGTVWDQDLQTCNHNFNNCSTGTESTTPKPPCEPATNGTTA 1363	6 CVRNNKGGFT	130	Дb
KEPAPTTTKS	2T	24	Qy
TARPVTARPTTSSPTTASSSQTTSPVTQAPNTDGKCRSEGFMADPNNCSKFYR 1305	PT	125	дb
PITIKSAPTTPKEPAPTTKEPAPTTPKEPAPTT 241	3 PKEPAPTTK	20	Qy
- PTTASTSRPSDQTSTSRP	1 SCGPGTVWDA	119	밁
PKEPTPTTPKEPASTTP	8	16	Qy
SSSSSSTSSKPNPSETCKVNGQFIGDRSDCAKFYRCVDNDRGGFNMVPF 1190	1 NNNNQGSSSS	113	Дb
PTSKVLA	9EKTS	13	Qy
SGGSSNQGSSSNSGS	SSSS	0 1071	Дb
VETKETTTTNKQTSTDGKEKTTSAKE	8 SLPF	8	γQ
KKYVSQGG	3 NHPD	102	DЬ
(PPVVDEAGSGLDNGDFKVTTPDTSTTQHNKV	8 NKKN	2	QΥ

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A Zhang Y., Moreno C., Singh M.;
Y "Cloning and characterization of a new member of the PGRS family that
Y Is a useful marker of polymorphism in Mycobacterium tuberculosis.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
Y EMBL, AFO71081; AAD41594.1;
Y REMBL, AFO71081; AAD941594.1;
Y RINTERPO; IPRO02951; Atrophin.
OR InterPro; IPRO02965; P_rich_extensn.
OR InterPro; IPRO02965; P_rich_extensn.
OR InterPro; IPRO02965; P_rich_extensn.
OR PRINTS; PRO1212; ATROPHIN.
OR PRINTS; PRO1217; PRICHEXTENSN.
OR PRINTS; PRO1218; PSTLEXYENSIN.
OR PRINTS; PRO1218; PSTLEXYENSIN.
OR PRINTS; PRO1218; PSTLEXYENSIN.
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Best Local Similarity 28.2
Matches 248; Conservative
                      558
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROLINE-RICH MUCIN HOMOLOG.
                                                                                374
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                                                                                                                                                                                314 PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

MCBI_TaxID-1773;
                                                                                                                                                                                                                                                                                                    257 PVPNKIPPAPP----APPVAVAAVLVAPCPPLPPLPNNHPPAPPAAPVPGVPLAPLPNSHP 313
                                                                                                                                                                                                                                                                                                                                                                 444 TTPKKLTPTTPEKLAP-----TTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTT-- 493
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LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPA-----PTTPKEPAPTTPKGTAPTTL 611
                                                         TTTTPALPAPIPPLPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP--
                                                                                                      --TTPKEPAPTTPKEPAPTTPKETA----PTTPKGTA----PTTLKEPAPTTP-KKPAPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 715; DB 2; 28.2%; Pred. No. 4.6e-40; tive 39; Mismatches 361
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ДĎ	ΔÃ	Db	δ,	, Db	Qy	DЬ	Qy	DЪ	Qy	Ъ	Qy	Дb
726	890	666	839	638	779	605	719	549	665	489	612	432
726 VPGAPLAPLPINGRPVFARKNSLIGSSSGDT 756	TSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGET 929	SMALPPAPPDPPTPLLATPPAPPAPPLPMSPPAPPLPPAAPDPPAPPLTINQPPSPPLAP 725	SKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP 889	638 PAAPPAPPAPPVRATTP655	779 TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN 838	PAPPAPPAPPSALPFVNPPA	KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI 778	PAPPAPPTPPKLLSANPPCPPVPPAPNRPPAPPAPPAPPAPPELPAPPDPPTPPVANSP 604	KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSP 718	Ą₽	KEPAPTTPKKPAPKELAPTTTKGP-TSTTSDKPAPTTPKETAPTTPKEPAPTTP 664	432PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP 488

Search completed: April 26, 2002, 16:28:53 Job time: 548 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1366
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sp_bacteria:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	؈	8	7	ð	U	4	ω	N	_	Result No.
703.5	703.5	706.5	707.5	715	781	784	812	814	817	846	863.5	891.5	946.5	982.5	1713.5	3759	7236	7265	Score
9.6	9.6	9.7	9.7	9.8	10.7	10.7	11.1	11.2	11.2	11.6	11.8	12.2	13.0	13.5	23.5	51.5	99.2	99.6	Query
5085	4880	6677	555	763	2112	1188	2187	1480	1315	1274	1489	1795	1049	1079	401	1054	1404	1404	Length
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
592.5	598.5	600.5	605	607.5	607.5	622.5	627.5	628.5	629	631	632	633	636	643.5	647.5	649	653.5	660.5	661.5	664	665	665	667.5	680	695
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P91365 caenorhabdi	Q9sbml volvox cart	Q9nkc9 drosophila		Q99307 epstein-bar	-				001761 caenorhabdi			Q41707 vigna ungui	Q17362 caenorhabdi	Q91803 xenopus lae		Q99552 homo sapien		dros	homo		7 mus	-	Q9vpg1 drosophila	Q94185 caenorhabdi	057580 qallus qall

## ALIGNMENTS

RRA	RESULT OCCUPANT OCCUP
SEQUENCE FROM N.A.  Merberg D.M., Fitz L.J., Temple P., Glannotti J., Murtha P.,  FitzGerald M., Scaltreto J., Kelleher K., Preissner K., Kriz R.,  Jacobs K., Turner K.;  (In) Preissner K.T., Rosenblatt S., Kost C., Wegerhoff J.,  Mosher D.F. (eds.);  Biology of vitronectins and their receptors., pp.45-52,  Elsevier Science Publishers B.V. (1993).  [3]  SEQUENCE FROM N.A.  Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,  Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J.,  Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T.,  Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.  EMBL; U70135; AAB09089.1;  InterPro; IPR000585; Hemopexin.  InterPro; IPR000585; Hemopexin.  InterPro; IPR001212; Somatomedin_B.  InterPro; IPR001212; Somatomedin_B.  Ffam; PF01033; Somatomedin_B. 2.  PRINTS; PR00438; GFCYSKNOT.	1 92954; 92954; 1-FEB-11 1-FEB-11 1-FEB-11 1-JUN-22 1-JUN-22 1 1-JUN-22 1 1-J

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PROSITE; PS00024; HEMOPEXIN; UNKI
PROSITE; PS00524; SOMATOMEDIN_B;
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
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TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQV
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66; Conservative
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97.3%;
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Pred. No. 0;
0; Mismatches
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Best Local Similarity
Matches 1362; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                               Q9BX49;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updata
BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR
BG174L6.2.
                                                                                                                                                                            Submitted (JUL-2000) to the EMBL; AL133553; CAC36090.1; SEQUENCE 1404 AA; 151076
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 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIR
                                         KRVCTAELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP
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ilarity 97.0%;
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                           OTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                                                RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWDESVY
                                                                                                  RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
                                                               PQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN
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Best Local Similarity 55.0
Matches 779; Conservative
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PROSITE;
SEQUENCE
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"a novel mouse gene highly homologous to a megakaryocyte stimulating factor precursor
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MRNA, COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING
PRECURSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
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PS00524; SOMATOMEDIN_B; 2.
1054 AA; 115991 MW; 4FC64B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3759; DB 11;
Pred. No. 8.6e-237;
6; Mismatches 169;
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Sciurognathi; Muridae;
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AFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
                 AKYKDRPESVYFFKRGGNIQQYTYKQEPMKKCTGRRPAINYSVYGEAAQVRRRRFERAVG
                                                             AKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIG
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SUPERFICIAL ZONE PROTEIN (FRAGMENT).
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Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                  ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFE 1267
                                                                                                                                                                                          DYYALSKDQYYNIDVPSRTARAITTRSGQTLSNTWYNCP
                                                                                                                                                                                                                DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1366
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InterPro; IPR002965; P_rich_extensn. PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DB
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[2]
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Submitted (MA
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STRAIN-BRISTOL N2;
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Y51B11A.1 PROTEIN.
Y51B11A.1.
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investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                                                                                                                                                                268
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hes 332;
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ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTT
                    TTTAPETTSTEP-PSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPE-TTSTES
                                                                             PEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEP--APTTPKEPAPTTPKEPAPTTPK
                                                                SSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTSTEP----PSSSTTPVQTT
                                                                                                          APETTRTEPPSSSTTPVQNTTTTAPETTSTEPPSSSTTPVQTTTTT----APETTSTEPP
                                                                                                                       APTTIK--EPAPTITKSAPTTPKEPSPITTKEP-APTTPKEPAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                         QKELEIADCRANQTPHTMLP-----STLTSVDMETPSTLVLSSTPTSSSTPIKETT
                                                                                                                                                                                                                                                                                                                                                                                                QKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKV-----TTPDTSTTQ-HNKV
                                                                                                                                                     PSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTT
                                                                                                                                                                             PTAPKKPAPTTPKEPAPTTPKEP-----
                                                                                                                                                                                               TTTTAPETTSTESPSSSTTPVQTTTTTAPETTSTEP-PSSSTTPVQTTTTTAPETTSTEP
                                                                                                                                                                                                                   TTKSAPTTEKEPAPTTEKKPAPTTEKEPAPTTEKEPAPTTEKEPAPTTEKEPA
                                                                                                                                                                                                                                          PSSSTSPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTTAPE---TTSTEP-PSSSTTPVQT
                                                                                                                                                                                                                                                              KEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPT
                                                                                                                                                                                                                                                                                    TAPETTSTEPPSSS----TSPVQTTTTTAPETTSTEAPSSSTTPVQTTTTTAPETTSTEP
                                                                                                                                                                                                                                                                                                   sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%;
                                                                                                                                                                                                                                                                                                                                -PSSSTTPVQTTTTTAPETTSTEAPSSSTTPVQTT-----TT
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                                                                                                                                                                                                                                                                                                                                                                                                                         131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oda; Chromadorea; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 982.5;
Pred. No. 5.3e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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723
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davles P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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16,
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                                                                                                                                              Miklos G.L.G.,
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RA HOSTID D., HOUSTON K.A., HOWLAND T.J., Wei M.H., IDEGWAM C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Sjendling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter T.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter T.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter T.C.;
RA FlyBase; FB90030561; CG5228.
SO SEQUENCE 1049 AA; 107278 MW; 954DD629E7619671 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAK---PTTLK----PTEGTSAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AETTTKGPALTTPKEPTPTTPKEPASTTPKEPT---PTTIKSAPTTPKEPA---PTTTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTSAKP----TTLKPTEGTSAKPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDNGDFKVTTPDTS--TTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIGTTAKPTTLKPTEGTSAKPTTLKPTEGTSAKPTTLKPT-----EGTTAKPTTLKPTE
                                                                   TLKPTKGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGT
                                                                                                                               TPKETAPTT - - PKKLTPTTPEKLAPTT - - PEKPAPTTPEELAPT
                                                                                                                                                                                               AKPTTLKPTEGTTAKPTTLKPTKGTKGTSAKPTTLK-PTEGTTAKPTTLKPTEGTTAKPT
                                                                                                                                                                                                                                                            KEPAPTTPKE---PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKE---PAPT
                                                                                                                                                                                                                                                                                                                            TTAK---PTTLKPTEGTTAK---PTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTT
                                                                                                                                                                                                                                                                                                                                                                                     TTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPA---PTTTKSAPTTPKEPSPTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTLKPTDGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTPKEPAPTTPKEPT--PTTPKEPAPTTKEPAPTTPKEPA---PTAPKKPAPTTPKEPAP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTTPKEPAPTTTKEPA---PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGTTAK - - - - PTTLKPTEGTTAKPTTLNPTEGTSAKPTTLKPTEGTTAKPTTLNPTEGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKPTEGTSAKPTTLKPTEG - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C., Gabrielian A.E., Garg N.S., Gelbart W.M., A., Gong F., Gorrell J.H., Gu Z., Guan P., Ha. N.L., Harvey D., Heiman T.J., Guan T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LKPTEGTSA-----KPTTLKPTE--GTTAKPTTLKPT---EGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 946.5; DB 5; Pred. No. 1.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480;
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                                                                                                                                      --TPEEPTPTTPEEPA
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiifer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA George J., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EG:56G7.1 PROTEIN.
EG:56G7.1 OR CG14796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTSAKPTTLKPTEGTTAKPT----TLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKPAPKELAPT-----TTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTP 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAEG-ETPHMLLRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRKPKTTPT----PRKMTSTMP-ELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPTTLKPTEGTSAKPTTLKPTE-GTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K--TITTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPK---KPT--STKKPKTMPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTK 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT---SAQPTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPTEGTTAKPTT----LKPT-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETAPTTPKEPAPTT--PKKPAPTTPETPPPTTSEVSTPTTTK-----EPTTIHKSPDE 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPTTLNPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PTTLKEPAPTTPK----KPAPKELAPTTTKGPTSTTSDKPAPTTPK 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045
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Best Local S
Matches 317
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EMBL; AE003421; AAF45644 1; -
EMBL; AL03102B; CAA19845 2; -
FlyBase; EBgn0025390; EG:56G7.1.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002557; Prich_extensn.
Pfam; PF01507; Chitin_bind_2; 2.
PRINTS; PR01217; PRICHEXIENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10
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SEQUENCE FROM N.A.
Cadieu E., Dreano S., Lelaure V., Mottler S., Galibert F.;
Cadieu E., Dreano S., Lelaure V., Mottler S., Galibert F.;
"Sequencing the distal X chromosome of Drosophila melanogaster.";
"Sequencing the distal X chromosome of Drosophila melanogaster.";
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999)
366 PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPT
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Local Similarity 27.0%;
hes 317; Conservative 15
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                                                                                                       TTPSTTTPST-----TTPSTTTPST-----TTPSTTTPSTTTTVKVSTHRPRTTSQKTT
                                                                                                                                                                                                                                                 TKRPTTVTEKTSSATEKPRTTVVTTTTQKRSTTTHNTSPDTKTTIRSTTLSPKTTTTPST
                                                                                                                                                                                                                                                                                          TTPKEPTPTTPKEPASTTPKEPAPTTTKSAPTTPKEPAPTTTK-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETPATAATTREPLNDINKYQYKRYTYGTDKNDVTEAPEIKSPL----KGLHLSENIVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTLEPSTAYHKYPAYPSYPSYEYSS--HHRGKERAAENLELEKEGVPRKLKLSENIVIQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGYSRDAT-CNCDYNCQ-----HYMEC---CP-----DFKR-VC-----TAAEV
                                                                                                                                                                                                                                                                                                                                                                                      PETTTT--TTTTKPVVLTCPTISPPDTTPKPSTTTAVTKSTPKISSTEQHSTTTAKTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITEEHSVSENQESSSSSSSSSSSSTIWKIKSSKNSAANRELQK-----KLKVKDN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTT
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Pred. No. 7.
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Db	624 TASTTTKKTTTSPKTTKTTDIPTSTTSKLSTTTQKTTTTHKETAATTSTEKPKTT 679
Qy	EPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTT
Дb	
Qy	TKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTP
Дb	TTTPQPTTTTTLTVTPKTS
Qy	PKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPK-ETAPT
Db	800 KVALITTOKETTPTQSTSTTIFTRKTTTNNPEPTSTEKPITSTTPKPSTTTPKTSTVASST 859
Qy	KLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTT
Db	860 EKTTISSPKPTTEKSTENPTTNSVKTSALTSSTQRATSTTSEPTKTT-QNITTTTPKPTT 918
Qy	PTTPKETAPTTPKGTAPTTLKEPA
DЪ	919 LKTSTQEATTSTQKVSTVTITTKKATESSPLTTLSTEEPNTTPKPLRTTTPTTTSVTATT 978
Qy	TTTKEPT STTSDKPAPTT
Дb	TSTQKPKSTTPTSTTRTTPKYTTVIVSTQNPTTTTSKTSTYTI 1
Qy	PKKPAPKELAP-TTTKGPTSTTSDKPAPTTI
DЬ	1036TTP-NPSPSTQRPTTTTRQPTSITASTTSIGTTRIPTTTNPQNSTSSTDLTTVTRPPC 1092
Qy	TSEVSTPTT-TKE
ф	1093 PDPDSTSDKNTNTACTQELQQVNLLELQSPQKQEQFTHTRTHTALTGSRNTLGGQEVPDY 1152
Qy	PKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETA
DЬ	1153 MDDAPSSAEAESGQATTAKAPTMSTLAAAHLLQKLFHIISTTPPSREHAPTQRPSSQP 1210
Оу	KITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVT:
Db	TAHSLRLSIQQLASTQKRSIPPKTLVTHN
Qy	TAKPKDRATNSKATTPKPOKPTKA-PKKPTSTKKPKTMPRVRKPKTTPTPRKMTS
DЬ	1270 ED-SETYDSETSEQYTDEDNEVLDKTQPRAMSSTTVAAVLPAVPSTTTEREPQK-TSSSP 1327
Qy	PTSRIAEAMLQTTTRPNQTPNSKLVEV
Db	1328SPTKATSSTTTQPIETTTGDLEYDSSGSSD 1357
S2 4	LT 8
	RELIMINARY; PRT; 1
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	ION SPECIFIC ACIDIC REPEAT
	infestans (Potato late blight fungus).
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	SEQUENCE FROM N.A.
	-11; ;
	R-1998) to the EMBL/G 5; AAC72308.1;
	1489 AA; 164037

Goernhardt B.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF061185; AAC72308.1; -SEQUENCE 1489 AA; 164037 MW; 764CC79D1C2F5163 CRC64;

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                                                                                                                                                                                                                                                                                     1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 TKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNK 166
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                                       EETTYAP----TEETTYEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGP 128
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LKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT 994
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	Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,	RA
	, Latreille P.,	RA S
	lo A., Fulton L.,	RA
	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	RA
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-PKPKEVSKEPPKPTEPPKP-AAPKKWKPPWEDDPDEPEADFTMPAPKKPDTEDP
                           TPKPQKPTKAPKKPTSTKKPKTMPRVRKPK-----
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                                                                                   TQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKAT
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Hohorst D., Gao M., Showalter A., Bedinger P.A.;
Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP159297; AAD55980.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR001998; XyJose_isom.
InterPro; IPR002965; P.rich_extensn.
InterPro; IPR003992; LRR, Out.
Pfam; PF00560; LRR; 3.
PRINTS; PR01217; PRICHEXTENNN
PFOSITE; PS001772; XYLOSE_ISOMERASE_1; UNKNOWN_1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl

Panicoideae; Andropogoneae; Zea.

NCBI_TaxID-4577;
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PPAPVSSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPPTPKSSPPLAPVSSPPQVE
                              PTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTP
                                                              APKSSSP-----PAPVS--SPPPLKSSPPPVPESSPPPTPKSSPPLAPVSSPPQVEKTSP
                                                                                           TTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA
                                                                                                                             SSPPPEKSLPPPTLTTSPPPQEKPTPPSTPSKPPPPSPVETLPPPSKSSPPEEPVSSPPQ
                                                                                                                                                        PAPTTPKE-PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPT
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Similarity 23.4%; Pred. No. 3.9e-45;
69; Conservative 109; Mismatches 490;
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Q9LIE8;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress)
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                             Kaneko T.,
Submitted (
1031
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                                                                                                            SEQUENCE FROM N.A. STRAIN=COLUMBIA; PubMed=10907853;
                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=COLUMBIA; Kaneko T., Kato T.,
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y y	42 TLAPKVTTTKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQKPTKAPKKPTST	Qy Db
TTLKTT:   	382 TERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITT :	Db
(DKT	825 TKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMT-TTAKD 	Qy
TPTT	774 STTSDKEPAPTTPKETAPT-TPKEPAPTTPKEPAPTTPETPPPTTSEVSTP	Qy Db
PPI -	715 TPKGTAP-TTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKG 	Qy Db
APT   TAT	660 PTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPA	Qy Db
PA PA	604 PTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKE 	Qy Db
PA PA	S55 -APTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK	Qу
PY    -	501 PTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKE 	Qy Db
PA PV	445 APTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKE 	Qγ
TP — EP	389 SAPTIP-KEPAPTIPKKPAPTIPKEPAPTIPKEPIPTIPKEPAPTITE-KE 	Qу Дъ
1-1	350 SAPTTEKEPAPTTTPTTT	Qу Db
× – ×	299 TITKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTT ;   ;	Qy Db
AK AK	STQSIEKTSAKDLAPTSKVLAKPTPK 	Qy Db
LTV	181 VDEAGSGLDNGDFKVTTPDTSTTOHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSL'   :	Qy Db
PV P-	123 SENQESSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKP	Qy Db
ASI	66 AAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKKKKVIESEEITEEH   :	Qу
Ga	uery Match 11.2%; Score 814; DB 10; Length 1480; set Local Similarity 28.8%; Pred. No. 6.9e-45; Indels 212; atches 329; Conservative 61; Mismatches 541; Indels 212;	Que Bes Mat

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RESULT P706700 P706700 P7 P70670 P7 P7 P7 P7070 P7 P7 P7070 P7 P7070 P70
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A YOLOW M.V., St-Arnaud R.;

"lifferential splicing-in of a proline-rich exon converts alp

"nifferential splicing-in of a proline-rich exon converts alp

"note a muscle-specific transcription factor.";

Genes Dev. 10.1763-1772(1996).

R EMBL; U48364; AAB18734.1;

R EMBL; U48364; AAB18732.1;

R EMBL; U48363; AAB18732.1;

R MCD: MC3:106095; NACC.

InterPro; IPR002715; NAC.

InterPro; IPR003037; TS-N.

Pfam; PF01849; NAC; 1.

Pfam; PF02094; TS-N; 1.

CECUTEMORE 7187 AA. 220599 MW: 003646AA8664DEBFD CRC64;
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Matches
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220).
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                                                                                                                                               QHV---PPTSPPKSPVSDTLSGALTSPPPKGPPATLAETPTYPKKSPKPAASKKTPATPS
                                                                                                                                                                                                                                                                                              T-----TVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKA
                                              PEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKRAPKTAVSKEIPSKGVTAVPLEISLP 1057
                                                                                                                                                                                ETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKE-PAPTTTKSAPTTPK 356
                                                                                                                                                                                                                                               TLATSIPKVTSPSPQKTPKSVSLKGAPAMTSKKAT---EIAASKDVSPSQ--FPKEVPLL
                                                                                                                                                                                                                                                                                                                                                                                    GDFKVTTPDTSTTQHNK-----VSTSPKITTAKPINPRPSLPPNSDTSKETSL--TVNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                             KTPEVTASRLISAVQSPKVDPIMSD-----VTPTSPKKTSATAVPK--------
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11; Conservative
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-TPKEPAPTTPKK-PAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKE
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Pred. No. 1.4e-44;
8; Mismatches 449
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Sciurognathi; Muridae;
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SEQUENCE FROM N.A.
STRAIN-B73; TISSUE-POLLEN;
STRAIN-B73; TISSUE-POLLEN;
STRAIN-B73; TISSUE-POLLEN;
Rubinstein A.L., Broadwater A.H., Lowrey K., B
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ
EMBL; Z34465; CAAB4230.1; -
Mendel; 14346; Zeama;2336;14346.
TERRO01611; LRR.
                                                                                                                                                                                                               Q41805 PRELIMINARY; PRT; 1188 AA. Q41805; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation extensin-like Protein Precursor.
                                                                                                                                                      Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
Panicoideae; Andropogoneae; Z/
                                                                                                                                                                                                     Zea mays (Maize)
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                                                                                                                                                                                                                                                                                                                                                                                               PRKMTSTMPELNPTSRIABAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPT 1013
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                                                                            Bedinger P.A.;
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01-MAY-2000
01-MAY-2000
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CG4090 PROTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTTKKPAPTAPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP--PKEPVSSPPQTP----KSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK
                                                                                                                                                                                   MSSPPPPEVKSPPPPAPVSSPPPPPVKSPPPPAPVSSPP----PPVKSPPPPAPVSSPPPPV
                                                                                                                                                                                                                                                                                                               LKE---PA-----PTTPKK---PAPKELAPTTTKE---PTSTTSDKPAPTTPKGTAPTTP 724
                                                                                                                                                                                                                                                                                                                                            PTTVISP-PSEPKSSPPPTPVSLPPPIVKSSPPPAMVSSP-PMTPKSSPPPVVVSSPPPT
                                                                                                                                                                                                                                                                                                                                                                     PTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPLSSPPPAPQVKSSPPPVQVSSP-PPAPKSSPPLAPVSSPPQVEKTSPPPAPLSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230;
                                                                                                                                                        SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET
                                                                                                                                                                                                                                                              -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
                                                                                                                                                                                                                                                                                          VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA----PKSSPPPAP
                                                                                                                                  SPPPAP--
                                                                                                                                                                                                           -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTKEPTT1HKSPDESTPEL 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
 PROTEIN.
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                          (TrEMBLrel.
               (TrEMBLrel.
                                                                  PRELIMINARY
                                                                                                                                  -VKPPSLP-PPAPVSSPPPVVTPAPPKKEEQSLPPPAES
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Pred. No.
               Created)
Last sequence update)
Last annotation update)
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RA Abril J.F., Agbayani A., Au B., Charks, C., Beasley E.M., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Bersts K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davles P., Ra Cherry J.M., Cawley S., Dahlke C., Daveport I.B., Dietz S.M., Ra Chodek R., Cong F., Gorrell J.H., Gu Z., Guan P., Heischmann W., Ra Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyam C., Ra Liasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., Ra Ra Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A., Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Ra Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Pivrasa R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ra Manja S.M., Woodage T., Woolbey K.C., Wu D., Yang S., Yao Q.A., Ra Miliams S.M., Woodage T., Woolbey K.C., Wu D., Yang S., Yao Q.A., Ra Miliams S.M., Woodage T., Woolbey K.C., Wu D., Yang S., Yao Q.A., Pache J., Shen H., Shen J., Shen M., Shon S., Zhu M., Shing G., Zhao Q., Zheng L., Shen H., Shen J., Shen M., Shen G., Zhan M., Shen G., Zhan M., Shen J., Shen
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0038492; CG4090.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR000561; EGF-like.
pfam; PF01607; Chitin_bind_2; 10.
SMART; SM00494; ChtBD2; 11.
1077
                                               165
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                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                              NCSKFYRCVDNGKGGFTKVSF---TCPPNTLWDPEANSCNHPDQIQTK-----PLKCK 1036
                                                                                                                                                                                                                                              NCQHYMECCPDFKRVCTAAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTK 108
                                          {\tt NKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRP}
                                                                                                                                            KVI----ESEEITEEHSVSENQESSSSSSSSSSSTIKKIKSSKNSAANRELQKKLKVKD 164
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A; 219547 MW;
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27.3%;
  -GSSSNTGSSSNSGASSSGGSSNQGSSS
                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                                                                                                      Score 781; DB 5;
Pred. No. 1.4e-42;
8; Mismatches 367
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   Q9XDH2;
Q9XDH2;
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                                                                                                                                                                                                                                                          QVYAFKCGKGTVWDTSTETCNYADQVSGN------CSSGQTTTPGTTTEPGTTES
                                                                                                                  PTTTE----
                                                                                                                                   ITTTEIMNKPEETAKPKORATNSKATTPKPQKPTKAPKKPTSTKKPKTMP
                                                                                                                                                                                                           TTSSGKP----ETTSKAPEN-----TTTWA---PETTTT------SSPETT
                                                                                                                                                                                                                             KPEPTTTTESPESSTPEGSVTTLQPEPQPNYNCSSEGFFPDPEDCSRYYRCVDAAKNGKY
                                                                                                                                                                                                                                                                                                                                    EPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKK-----PAPKELA-----PTTTKGPT
                                                                                                                                                                TT---VASETTTTTSGT-----
                                                                                                                                                                                                                                                                                                                                                                                   PTTPK--GTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPK 725
                                                                                                                                                                                                                                                                                                                                                                                                            TTEEPTPEKPQKPT-TTEYPQKPTTTEEPTPEKPQKPTTTEYPQKPTTEEPTTTSIPGYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCSKLPAEPITTTPSEESKDPGSTTPQST 1557
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  (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 17,
                                                      PRELIMINARY;
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Last sequence update)
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                                                                                                             ---SPAPSTNTSAP-----CPETGP
                                                                                                                                                           -TTTATPETTTKPPKP-----ETTTIAGEETSTSKS
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"Cloning and characterization of a new member of the PGRS family that is a useful marker of polymorphism in Mycobacterium tuberculosis.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AFO71081; AAD41594.1;
InterPro; IPR002951; Atrophin.
InterPro; IPR002952; P_rich_extensn.
InterPro; IPR003882; P_istil_extensin.
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PRINTS; PRO1218; PSTLEXTENSIN.
SEQUENCE 763 AA; 75034 MW;
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                                                                                                               TKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNK
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            TSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP
                                                                                      PTTPKEPAPTTPKEPTTTTPKEPAPTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPK
                                                                                                                                                                                        PTTPKEPAPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPK
RTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPK
                                                               TSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOMATOMEDINB.
; HEMOPEXIN; UNKNOWN_1
; SOMATOMEDIN_B; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                         151090 MW;
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 7410;
Pred. No. 0;
0; Mismatches
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В
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Best Local Similarity 99.0
Matches 1376; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BX49 PRELIMINARY; PRT; 1404 AA.
Q9BX49; 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR).
BG174L6.2.
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                                                                                                                                                                                                                                                                                                                                                                                                              Wray P.;
Submitted (JUL-2000) to the
EMBL; AL133553; CAC36090.1;
SEQUENCE 1404 AA; 151076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKK
                                                                                                                                                                              DCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKK
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                                                                                                                                                                                                                                                                                                                                     99.6%;
99.7%;
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Pred. No. 0;
0; Mismatches
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                    FRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIK
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                                                                                                                                                                                                     KPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGET
                                                                                                                                                                                                                                                 GLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
                                                                              DAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGR
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Best Local S
Matches 795
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EMBL; AB034730; BAA92310.1; -.
MGD; MGI:1891344; Brg4.
InterPro; IPR000585; Hemopexin.
InterPro; IPR000585; P_rich_extensn.
InterPro; IPR001212; Somatomedin_B.
Pfam; PF0103; Somatomedin_B; 2.
PFINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00022; SOMATOMEDINB.
SMART; SM00120; HX; 2.
SMART; SM00120; HX; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00024; SOMATOMEDIN_B; 2.
SEQUENCE 1054 AA; 115991 MW; 4FC64BFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09JM99;
01-OCT-2000
01-OCT-2000
01-JUN-2001
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"a novel mouse gene highly homologous to a
megakaryocyte stimulating factor precursor
zone protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66ML60
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PAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTT
                                SLAPNSETSKEASLASNKETTVETKETTATNKQSSA-SKKKTTSVKETRSAEKTSDKDV-
                                                                                                                  SLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLA
                                                                                                                                                 KNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPDPPTTPHSKVATSPKTTAAKPVTPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-2000 (TrembLrel. 15, Created)
T-2000 (TrembLrel. 15, Last sequence update)
N-2001 (TrembLrel. 17, Last annotation update)
COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING
RSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
                                                                                                                                                                                                                                                                                                                                  _Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; (
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  52.8%;
                     ----LPQEPEPTTAKEPPPTTKKPEPTTRKEPEPTTPKE
                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                     Score 3913; DB
Pred. No. 4.6e-
57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                            4FC64BFA42283235
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                                                               EPTSTTPK ----
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..6e-245;
les 166;
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and cartilage
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                        374;
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RESULT
077765
ID 07
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                                                                                     GQTLSKIWYNCP
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                                                                                                                                   LHNEVKVSTMWRGFPNVVTSAITLPNIRKPDGYDYYAFSKDQYYNIDVPTRTARAITTRS
                                                                                                                                                 LHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDVPSRTARAITTRS
                                                                                                                                                                                  KQEPMKKCTGRRPAINYSVYGEAAQVRRRRFERAVGPFQTHTFRIHYSVPMRVSYQDKGF
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                          PRELIMINARY;
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Best Local S
Matches 320
                                                             Q9N4S7; PRELIMINARY;
Q9N4S7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
Y51B1la.1 PROTEIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOY-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) SUPERFICIAL ZONE PROTEIN (FRAGMENT).
                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
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Schumacher B.L., Hughes
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EMBL; AF056218; AAD13404.1;
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NCBI_TaxID=9913;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                 TEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVA
                                                                                                                                                                                          DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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Hughes C.E.,
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                      oda; Chromadorea;
Caenorhabditis.
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24; Mismatches
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annotation update)
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                                   Rhabditoidea;
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STRAIN-BRISTOL N2;
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                       APE---TTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPS
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29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 982.5; |
Pred. No. 1.4e
31; Mismatches
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -STLTSVDMETPSTLVLSSTPTSSSTPIKETT
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RX MEDLINE=**CLYDBUND; PULMBEUT-LV/JLIJA;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M.K., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
                                           ACCOMPAGNATION ACCOMP
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Q917S1;
01-MAR-2001 (Tr)
01-MAR-2001 (Tr)
01-JUN-2001 (Tr)
CG5228 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTTTITAPETTSTEPPSSSTTPVQTTTTTAPET---TSTEP---PSSSTTPVQTTTTTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAG 1074
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A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong M., Zhu S., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong M., Zhu S., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong M., Zhu S., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong M., Zhu S., Zhu X., Smith H.O.,
B Sequence 287.2185-2195(2000).
B EMBL, AE003495; AAG22353.1; -
B EMBL, AE003495; AAG22353.1; -
B EMBL, AE003495, AAG22353.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLKPTDGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEG
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                                                                                                                                         TAKPTTLKPTEGTSAQPTTLK---PTEGTSAQSTTLKPTEGTTAK---PTTLK---PTEG
                                                                                                                                                                                     PTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTP
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                                                 TSAQPTTLKPTEGTTAKPTTLKPTEGTSAK--PTTLKPTEGTTAK--
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                                                                              TIKEPISITSDKPAPTIPKGTAPTIPKEPAPTIPKEPAPTIP
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Pred.
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       KPAPKELAPTTTKGPTSTTSDKPAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PTTIKSAPTTPKEPA---PTTTKS
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H.O.,
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RESULT
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RA Addams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X., Pfelfer B.D., RA George R.A., Lewis S.E., Rander M.D., Zhang Q., Chen L.X., RA George R.A., Barand J.R., Yandell M.D., Zhang Q., Chen P. X., Chen P., RA Durlon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfelfer B.D., RA Harlis M.C., Basu A., Baxendale J., Helt G., Nelson C.R., Miklos G.L.G., Rander J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bacson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Becson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., M., RA Gebart W.M., Glasser K., Dunn P. Dodson K., Dupl L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W. RA Godser C., Gabriella A.E., Garg N.S., Gelbart W.M., Glasser K., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Lai Z., Ra Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lia X., RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lia X., RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lia X., RA Mount S.M., Molson K.A., Non K., Nosokern D.R., Pacleb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  076894;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
EG:56G7.1 PROTEIN.
EG:56G7.1 OR CG14796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Fleischmann
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                    Reese M.G.,
                                                           D.L.,
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Matches 330; Conserv
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EMBL; AL031028; CAA19845.2;
FlyBase; FBgn0025390; EG:56G7.1.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; Chitin_bind_2; 2.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spreadling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., M.D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng J., Zhou X., Zhu S., 
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                                                                                                                                                                                                    535
                                                                                                                                                                                                                                                                                                           475
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Cadleu E., Dreano S., Lelaure V., Mottier S., Galibert F.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364
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TTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPA 459
                                                                                                                            EPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTK-EPAPTTPKEPAPTTTKEPAPT
                                                                                                                                                                                 TVVTTTTQKRSTTTHNTSPDTKTTIRSTTLSPKTTTTPSTTTPSTTTPST----TTPS
                                                                                                                                                                                                               TSAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTIKGPALTTPKEPTTTPKEPASTTPK 340
                                                                                                                                                                                                                                                                                       PTISPPDTTPKPSTTTAVTKSTPKISSTEQHSTTTAKTTTTKRPTTVTEKTSSATEKPRT
                                                                                                                                                                                                                                                                                                                                                                                           YKRYTYGTDKNDVTEAPEIKSPL-----KGLHLSENIVILPETTTT--TTTTTKPVVLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEYSS--HHRGKERAAENLELEKEGVPRKLKLSENIVIQPETPATAATTREPLNDINKYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDLSSCAGRC-----GEG-YSRDATCNCDYNC----QHYMECCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSSTIWKIKSSKNSAANRELQK-----KLKVKDN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEDDYDTGAREQQPALKSEKLQVAAEGFEKPSLNVVVLQTTTLEPSTAYHKYPAYPSYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFSPVERKCLPGDQCPSTEISDSGSYIPQNCELKFPECAEEGTFRSPTDCALYYTCRLQE
                                                                                                                                                                                                                                                                                                                                                       KPINPRPSLPPNSDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTYLQTREKCPGSNSFDLERKLCRPRSEVDCFDFVPGPVQVPYAPQPYYPPYPAAPPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-----CCPDYESFCAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DFKRVC-----TAELSCKG------RCFE--SFERGRECDCDAQCKKYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESFNASSGRCVQHVPQHRPDHRPPQCQKEGRFPHPHDCKVYYRCDKNRTQPWLFACPAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PSGASQ---TIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSS
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                                                                             -TTPSTTTPSTTTTVKVSTHRPRTTSQKTTTASTTTKK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 902; DB 5;
Pred. No. 3.8e-50;
3; Mismatches 537
                                                                                                                                                                                                                                                                                                                                         SKETSLTVNKETTVETKETTTTNKQTSTDGKEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07F10C129BD9557B
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          Goernhardt B.;
Submitted (APR-1998) t
EMBL; AF061185; AAC72:
SEQUENCE 1489 AA; J
                                                                                                                                                                                                                                                                                    096449 PRELIMINARY; PRT; 1489 AA.
096449; 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. ACIDIC REPEAT PROTEIN PCAR90.
                                                                                                      SEQUENCE FROM N.A.
STRAIN-RACE 1-11;
                                                                                                              STRAIN-RACE
                                                                                                                                                                                                                                Eukaryota; stramenopiles;
                                                                                                                                                                                                                                                  Phytophthora infestans (Potato late blight
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                                                                                                                                                                                     NCBI_TaxID=4787;
                                                                                                                                                                                                             Phytophthora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETTTGDLEYDSSGSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVLDKTQPRAMSSTTVAAVLPAVPSTTTEREPQK-TSSSP--SPT----KATSSTTTQPI 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKPTKA-PKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTMSTLAAAHLLQKLFHIISTTPPSREHAP--TQRPSSQPSSSQRSR-GVTIAQMARHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEMTTTAKDKTTER----DLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT
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3; AAC72308.1; -
9 AA; 1622
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                                                                                                                                                                                                                                Oomycetes;
       MW;
                                                  EMBL/GenBank/DDBJ databases
  764CC79D1C2F5163 CRC64;
                                                                                                                                                                                                                             Pythiales;
                                                                                                                                                                                                                                             fungus
                                                                                                                                                                                                                                                                                                 PRECURSOR
                                                                                                                                                                                                                          Pythiaceae,
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121 TKKVIESEITEBESVENOESSESSESSIKKIKSSKNSANNELOKKKYKNA  282 TETVOYSTEETEGOHVIGGYEPSDETEAPTEGTTY - VPREETTAAPSET
21 TKKVIESEITEEHSVSENQESSSSSSTIWKI
21 TKKVIESEITEEHSVSENQESSSSSSTIWKI
21 TKKVIESEITEEHSVSENOESSSSSSTIWKI
21 TKKVIESEITEEHSVSENQESSSSSTIWKI
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(Costally-BRISTOL N2;

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Best Local Similarity
Matches 313; Conserv
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Q20007;
Q1-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
COSMID F35A5.
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STRAIN=BRISTOL N2;
Waterston R.;
Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
SUBMITTED (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U46675; AAB52641.1;
SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C1799F CRC64;
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                                                                        143
   245
                                                                                                                                             185 PSPKKAAPSKEHDPIVPPTPIKNPAKKWKPPWEDDEVPTEEIKEPEPATRKVPALKKKEP
                                                                                                                                                                                                              90 PSSKKAPPPSGASQTIKSTTKRSP----KPP---NKKKTKKVIESEEITEEHSVSENQES 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNQGINGIGVENKVRYNNAG 1420
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                                                 SSSSSSSSTIKKIKSKNSAANRELOKKLKVKDNK-KNRTKK-KP-----TP-----
   STSVKPVSDPSPTKKV-----
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27.68;
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                                                                                                                                                                                                                                                                                                          119;
                                                                                                                                                                                                                                                                                                  Score 846; DB 5; 1
Pred. No. 1.1e-46;
19; Mismatches 455;
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       -PVKKEPEVPPTPIKNPTKKWKPPWEDETPVEEVK 294
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                                                                                                  TPKPQKPTKAPKKPTSTKKPKTMPRVRKPK-----TTPTPRKMTSTMP
                                                                                                                               PSKKPDTEDPADPLG-----GPKTKDPK-----LNKKAPAEKPTEK---
                                                                       - PKPKEVSKEPPKPTEPPKP-AAPKKWKPPWEDDPDEPEADFTMPAPKKPDTEDP
                                                                                                                                                        TQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTTTTEIMNKPEETAKPKDRATNSKAT
                                                                                                                                                                                                                                                                                                                                                           PSPKKAVPE--KEPAKVAAKPRDLSPKKAIPIPANTQEAPPTPVKNPVKKWKPPWEDDDE
                                                                                                                                                                                     LSKKAPVEKPKPTTDPKDDKLKPSPAKKPEKAPEPAAPKKWKPVWDDDPDEPEADFTVPA
                                                                                                                                                                                                               AT-----KPEMTTTAKDKTTERDLRTTPETT--TAAPKMTKETATTTEKTTESKITATT
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           PRELIMINARY;
        PRT;
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Hohorst D., Gao M., Showalter A., Bedinger P.A.;
"Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF159297; AAD55980.1; -.
R Interpro; IPR001511; LRR.
Interpro; IPR001998; Xylose_isom.
Interpro; IPR002965; P_rich_extensn.
Interpro; IPR002965; P_rich_extensn.
Interpro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 3.
PFAMTS; PR01217; PRICHEXTENSN.
R PROSTE; FS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SMART; SM00370; LRR; 3.
SEQUENCE 1315 AA; 134401 MW; 64C97A2A01F0936F CRC64;
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Best Local (
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Matches 265; Conserv
817 PPQVEKTSPPPAPVSSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPLEPKPSSPPS
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TISSUE-POLLEN;
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                              APTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTT
                                                              LKSSPPPVPESSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPPTPKSSPPLAPVSS
                                                                                           TTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEP
                                                                                                                                                  EPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEASAPT
                                                                                                                                                                                    ASPPPLMKSPPPPAPVASPPQPLKSPPPPVLWLSTPSVKSPPPPVPVASPPPPVKSPPPL
                                                                                                                           PTPPSTPSKPPPPSPVETLPPPSKSSPPEEPVSSPPQAPKSSSP-----PAPVS--Sppp
                                                                                                                                                                                                           TTKSAPTTPKE----PAP--TTP----KKPAPTTPKEPAPTTPKE-PTPTTPKEPAPTTK
                                                                                                                                                                                                                                                                                    KSAPTTPKEPAPTTTKSAPTTP-KEPAP-----TTTKEPAPTTPKEPAPTTTKEPAPT
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                                                                                                                                                                                                                                                                                                                    -VLPPPAKTPSPPAPV-ASPPPEAPVSSPQPQVKSPPPPAPVASPPPPMKSP---PPPARV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 816; DB 10;
23.5%; Pred. No. 9.9e-45;
tive 106; Mismatches 486;
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Last sequence update)
Last annotation updat
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_	QY 85 NPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSS 144	
	Query Match 11.0%; Score 812; DB 11; Length 2187; Best Local Similarity 27.4%; Pred. No. 3e-44; Matches 311; Conservative 128; Mismatches 449; Indels 246; Gaps 51;	
	S L L L L L S	
	RP SEQUENCE FROM N.A.  RX MEDLINE=96312450; PubMed=8698236; RA YOTOV W.V., St-Arnaud R.; RA Toliferential splicing-in of a proline-rich exon converts alphaNAC RT into a muscle-specific transcription factor."; RT into a muscle-specific transcription factor."; RI Genes Dev. 10:1763-1772(1996). DR EMBL; U48364; AAB18734.1; DR EMBL; U48363; AAB18732.1; DR EMBL; U48363; AAB18732.1;	
	PRELIMINARY;	
	Qy 1072 DAGGAEGETPHMLLRPHVFMPEVTPDMDXLPRVPNQGIIINPMLSDE 1118 :	
	QY 1012 KPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSE 1071	
	QY 952 LKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPKPOKPTKAPKKPTSTK 1011  Db 1204PPPPAPMSSLPPPVKSPPPPAPVSSPPPPMKSPPPPAPIS 1242	
·	QY 897 ERDLRTTPETTTAAPKMIKETATITEKTIESKITATITQVTSTTTQDTTPFKITT 951	
	QY 837 TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTT 896	
	QY 783 TKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP 836  1051 SPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTLVSSPPPAPKSLPPP 1110	
	QY 733 TAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT 782	
	QY 689 APTILKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKG 732    I	
0 1	QY 629 PEEPTPTTPEEPAPTTPKAAAANNTPKEPAPTTPKEPAPTTPKETAPTTPKGT 688  .   :       :	

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1731

----ATTLPSLKEASVLS------PTATSSGKDSHISPVS-DACSTGTTTP 1770

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Best Local :
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DNA Res. 7:217-221(2000).
EMBL, APO01306; BAB03062.1; -...
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
DIACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Q9LIE8;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 17, Last annotation update)
S1MILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Kaneko T., Kato T.,
Submitted (MAR-2000)
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APTTTKSAPTTPKEP--SPTTTKEPAPTTPKEPAP---TTPKKPAPTTPKEPAPTTPKEP
                          PPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPPTAT---PPVAKPP
                                                 PAPTAPKKPAPTTPKEPAPTTPKEPAPTTT----KEPSPTTPKEPAPTTTKSAPTTTKEP
                                                                             --PPVTPIAQPPVATPPTATPPVATPPIATPPTSKSPISTPPISESPVATPPTATSPIKT
                                                                                                KSAPTTP-KEPAPTTPKKPAP--TTPKEPAPTTPKEPTTPTPKEPAPTTREPAPTTP-KE
                                                                                                                                KPPVTTP----PTTTPPIAKPPIATPPISTPPAATPPATTPPITTLPPAKPPVAISPIVT
                                                                                                                                                                                    KSPVATPPIATPPTATPPITIPPVATPPITTPPIANPPIIMPPIATPPVAAPPITNPPIS
                                                                                                                                                                                                              ETTTKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTPKEPAPTTT-----
                                                                                                                                                                                                                                                                 VNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV--LAKPTPKA
                                                                                                                                                                                                                                                                                                                   VVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLT
                                                                                                                                                                 KSAPTTPKEPAPTTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               330;
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30; Conservative
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EMBL/GenBank/DDBJ databases.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana chromosome (4,251,695 bp covered
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RESULT
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    STRAIN=B3; TISSUE-POLLEN;
Rubinstein A.L., Broadwater A.H., Lowrey K., Bed
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ da
EMBL; 234465; CAA84230.1; -
Mendel; 14346; Zeama;2368;14346.
InterPro; IPRO01611; LRR.
InterPro; IPRO03592; LRR_out.
Pfam; PF00560; LRR; 3.
SMART; SM00370; LRR; 4.
                                                                                                                                                                                                    Q41805 PRELIMINARY; PRT; 1188 AA. Q41805; Q41805; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-WOV-1996 (TrEMBLrel. 10, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) EXTENSIN-LIKE PROTEIN PRECURSOR.

Zea mays (Maize).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta Eukaryota, Viridiplantae; Fillionetiae; Poales; Proceedings (Maize).
Signal
                                                                                                                                                                  Spermatophyta; Magnoliophyta; L
Panicoideae; Andropogoneae; Zea
NCBI_TaxID=4577;
                                                                                                                                           SEQUENCE FROM N.A.
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yta; Liliopsida;
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a; Poales; Poaceae;
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SEQUENCE
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Q9VEL9;
01-MAY-2000
01-MAY-2000
01-JUN-2001
CG4090 PROTE
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    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                     1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPPVKSP--PPPTLVASPPPPVKSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPASPPAHVSSPPEVVKPSTP--PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPKETAP----TTP----KKLTPTTPEKLAPTTPEKPAP----TTPEELAPTTPEEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP--PKEPVSSPPQTP----KSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK
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                                                                                                                                                                                                                                                                                                                                                                                 LKE---PA----PTTPKK----PAPKELAPTTTKE---PTSTTSDKPAPTTPKGTAPTTP
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                                                                                                                                                                                                                                                                                                                              - KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
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                                                                                                                                                                                                                                                 KSPPPPAPISSPPPPVKSPPPPAPVS--SPPPPVKSPPPPAPVSSPPPPIKSPPPPAPVS
                                                                                                                                                                                                                     SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET
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                                                         PROTEIN.
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120980
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17,
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Last annotation updat
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Pred. No. 1e-42;
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       Tracheata; Hexapoda; Ins
ota; Diptera; Brachycera;
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                      Insecta;
           Muscomorpha;
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A Harris N.L. Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Weah M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A McIntola N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nelson K.S., Sunders R.D.C., Scheeler F., Shen H.,
A Nelson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
A Nelson D.R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wenty J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Yen J., A Nordey E.M., Rubin G.M., Venter J.C.,

"The genome sequence of Drosophila melanogaster.";

"Expart. A Neroza J.R., Lin M., A Neroza J. J. S.,
Lectore 287:2185-2295(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PlyBase; FBgn0038492; CG4090.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002561; EGF-like.
Pfam; PF01607; Chitin_bind_2; 10.
SMART; SM00494; ChtBD2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00022; EGF_1; 1. SEQUENCE 2112 AA; 219547 MW;
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                                                                 STSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTS 282
                                                                                                                                                                                                                                                                                                 IQTK---
                                                                                                                                                                                                                                                                                                                                                           STTKRSPKPPNKKKTKKVI----ESEEITEEHSVSENQESSSSSSSSSSSTIWKIKSSK 162
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           NSGSSSGSNSSGNQSTS----SSTSSSSSSNNNNQGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 782.5; DB 5
Pred. No. 2.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B91018E5551A5D36 CRC64;
                                                                                                                                                              GSSSNTGSSSNSGASSSGGSSNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369;
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Martens

that .";

Mycobacterium

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RESULT 15
Q9XDH2
ID Q9XDH2
AC Q9XDH2
DT 01-NOV
DT 01-JUN
                     Q9XDH2;
01-NOV-1999
01-NOV-1999
01-JUN-2001
                                                                                           Q9XDH2
                                                                                                                                                                                1930
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                                                                                                                                                                             CPETGP 1935
                                                                                                                                                                                                             KPKTMP 1017
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                                                                                                                                                                                                                                                                                                                                                                          QTTTPGTTTEPGTTESTTSSGKP----ETTSKAPEN-----TTTWA---PETTTT-
                                                                                                                                                                                                                                                                                                                                                                                                EVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CSRYYRCVDAAKNGKYQVYAFKCGKGTVWDTSTETCNYADQVSGN-----CSSG
                                                                                                                                                                                                                                            -ETTTIAGEETSTSKSPTTTE----
                                                                                                                                                                                                                                                                                                            LPSTTTDAIQEPTTSKKPEPTTTTESPESSTPEGSVTTLQPEPQPNYNCSSEGFFPDPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPTTEEPTTTSIPGYNPTTTSVPGYNPTTTPIPVETTTSTPGYK---PTTTGEPITTTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT-PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LA-----PTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPAPTTPKETA-----PTTPK--GTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPQKPT-TTEYPQKPTTTEEPTPEKPQKPT-TTEYPQKPTTTEEPTPEKPQKPTTTEYPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSEESKDPGSTTPQSTDEPTTVTKPI-TKPTE-EPSTEKPQKPTTQYPEKPTTTEE--PE 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P----KEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MADPEDCRKYYRCINAGASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCSKLPAEPITTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EPAP---TTPKK-----EPAP---TTPKKPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGLPFTTTGAQPTTTTLSSETETSTVTTSPESTTQPFSTTTMKFLPAGTECTGEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK---EPSPTTTKEPAP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P--PPTTTDLPPTSTTGLP-PTTTTELPPT----TTTDLPPTTTTRLPPTTTTSLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSIPEQCGAGTVWDQDLQTCNHNENNCSTGTESTTPKPPC--EPATNGTTATSTSSTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARPVTARPTTSSPTTASSSQTTSPVTQAPNTDGKCRSEGFMADPNNCSKFYRCVRNNKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKSAPTTPKEPAPTTKEPAPTTPKEPAPTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAQMQACNHAWAVKECGGIAPPTTSTPTTSR-PTTASTSRPSDQTSTSRPTGP----PTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKETQSIEKTSAK-DLAPTSKVLAKPTPKAETTTK-----:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TKEP----APT------TTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTT
                    (TrEMBLrel. 12,
(TrEMBLrel. 12,
(TrEMBLrel. 17,
                                                                                       PRELIMINARY;
            Created)
Last sequence update)
Last annotation update)
                                                                                     763
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                                                                                                                                                                                                                                                                                                          TTTATPETTTKPPKP----
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Best Local S
Matches 248
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Tahang Y., Moreno C., Singh M.;
Thang Y., Moreno C., Singh M.;
Teloning and characterization of a new member of the PGRS first a useful marker of polymorphism in Mycobacterium tubercul submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

In septon Jeno (JUN-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; AFO71081; AAD41594.1; -
R InterPro; IPRO02951; Atrophin.

R InterPro; IPRO02955; P_rich_extensin.

R InterPro; IPRO02965; P_rich_extensin.

PRINTS; PRO1221; ATROPHIN.

PRINTS; PRO1221; ATROPHIN.

PRINTS; PRO1217; PRICHEXTENSN.

PRINTS; PRO1217; PRICHEXTENSN.

PRINTS; PRO1218; PSTLEXTENSN.

PRINTS; PRO1218; PSTLEXTENSN.

PRINTS; PRO1218; PSTLEXTENSN.

PRINTS; PRO1218; PSTLEXTENSN.
870 KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI
                                                                                                                               489
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Mycobacterium tuberculosis.

Bacteria; Actinobacteridae;

Bactinomycetales; Actinobacterineae; Mycobacteriaceae; MCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                         257
                                                                                                                                                                                                                                                                                                                                                                                                                                           595
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                                               --PAPPAPPTPPKLLS--ANPPCPPVPPAPNRPPAPPAPPAPPELPAPPDPPTPPVANSP
                                                                                 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSAEPTPKA--LENSP
                                                                                                                  APPAPSMPSAVRVPPSPPIPPAPPAAPRASMPALPPAPPSPPATRLCPPLPPSPPAPNSP
                                                                                                                                                   KEPAPTTP----KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET----APTTPKEPAPTTP
                                                                                                                                                                                                                     LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPA-----PTTPKEPAPTTPKGTAPTTL
                                                                                                                                                                                                                                                     TTTTPALPAPIPPLPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP---
                                                                                                                                                                                                                                                                                        --TTPKEPAPTTPKEPAPTTPKETA----PTTPKGTA----PTTLKEPAPTTP-KKPAPKE
                                                                                                                                                                                    --PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP
                                                                                                                                                                                                                                                                                                                           PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL
                                                                                                                                                                                                                                                                                                                                                               ---PKAAAPNTPKEPAP-----
                                                                                                                                                                                                                                                                                                                                                                                            PVPNKIPPAPP---APPVAVAAVLVAPCPPLPPLPNNHPPAPPAAPVPGVPLAPLPNSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPPRPPAP-----PMPATPMEFPPLPPVPPDPISKETPPAPPAPPIPPAPVPIPPVPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTTTIKSAPTTPKEPAPTTTKSAP 366
                                                                                                                                                                                                                                                                                                                                                                                                                             TTPKKLTPTTPEKLAP-----TTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPPFPPAALNPPAP-----PAPPLANSPPLPPAPPTPAGT---PPAAPWPPVPAAPKSKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP--APTITKEPSPTTPKEPAPTITKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPTTPKEPTPTT----PKEPAPTTKEPAPTTPK-EPAPTTPKKEPAPTTPK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAP----TTTKKPAPTAPKEPAPTTPKETAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRPALPPCPPPPVVIPDPPEPAAPPVPPAPNSPPFPPPPPPAPKFVPAPPVP--PVPNSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCP--PAP----PAPPKPKSKAPFPPVPPAPPARELAPPLP--PAP-----PEAPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTPKEPAPTITKEPAPTTPKEPAPTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVP-----APRALAPLPPAPPAPAEPKSKPPFPPAP-----PAPPCWMLVSAAP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 715; DB
Pred. No. 1.9e
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the PGRS family
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Indels

232;

Gaps

39;

밁 Ş В ρ 망 Ş В Ş B Š 밁 Q 밁 õ 밁 Ş В ð 밁 õ 밁 õ 밁 õ В Ş 밁 Ş 밁 Ş В õ

869

548 815 488 708

762 431 313

644 256

658

201

90

929 604

В	Qy	Вρ	Qy	ДЪ	δÃ	ф
726	1041	666	990	638	930	605
1,	1041 TSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGET 1080	666 SMALPPAPPDPPIPLLATPPAPPAPPLPMSPPAPPLPPAAPDPPAPPLTINQPPSPPLAP 725	990 SKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP 1040	638 PAAPPAPPAPPAPPVRATTP	930 TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN 989	605PAPPAPPAPPSALPEVNPPAPPTPAAPKSRPAL 637

Search completed: April 26, 2002, 16:22:02 Job time: 507 sec

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
         protein -
                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       5698
5699
1048.5
9678.5
936.5
936.5
865.5
865.5
808.5
808.5
709.5
776
776
7739
7739
7739
7739
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7739
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5: sp_mammal:*
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8: sp_organel:
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11: sp_rodent:
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## ALIGNMENTS

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Q92954 PRELIMINARY; PRT; Q92954; O1-FEB-1997 (TrEMBLrel. 02, Created 01-FEB-1997 (TrEMBLrel. 02, Last se 01-JUN-2001 (TrEMBLrel. 17, Last an MEGAKARYOCYTE STINULATING FACTOR.
                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary Furner K.J., Giannotti J., Calvetti J., FitzGerald M., Kriz M., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesne Bhatla S., Kriz R., Hewick R., Clark S.C.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

InterPro: IPR000585; Hemopexin.

InterPro: IPR000585; Hemopexin.

InterPro: IPR001212; Somatomedin_B.

InterPro: IPR001212; Somatomedin_B.

InterPro: IPR001212; Somatomedin_B.

InterPro: IPR001212; Somatomedin_B.
Pfam; PF00045; hemopexin; 2. Pfam; PF01033; Somatomedin_B; 2. PRINTS; PR00438; GFCYSKNOT.
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Merberg D.M., Fitz L.J., Temple P., Giannotti FitzGerald M., Scaltreto J., Kelleher K., Prei Jacobs K., Turner K.;

(In) Preissner K.T., Rosenblatt S., Kost C., W Mosher D.F. (eds.);

Biology of vitronectins and their receptors., Elsevier Science Publishers B.V. (1993).
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Ikegawa S., Nakamura Y.;

"a novel mouse gene highly homologous to a hum megakaryocyte stimulating factor precursor and zone protein.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AB034730; BAA92310.1; -

MGD; MGI: HB91344; prg4.

R InterPro; IPR000585; Hemopexin.
R InterPro; IPR000585; P_rich_extensn.
R InterPro; IPR0002965; P_rich_extensn.
R InterPro; IPR0001212; Somatomedin_B.
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R Pfam; PF01033; Somatomedin_B.
R Pfam; PF00022; SOMATOMEDINB.
R PRINTS; PR00120; SOMATOMEDINB.
R SMART; SM00120; HX; 2.
R SMART; SM00120; HX; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JM99 PRELIMINARY; PRT; 1054 AA. Q9JM99; Q1-Q2T-2000 (TrEMBLrel. 15, Created) Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update) Q1-QCT-2000 (TrEMBLrel. 17, Last annotation update) Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update) MRNA, COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING PRECURSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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         4FC64BFA42283235 CRC64;
                                                                                                                                                                                                                                                                                                                                           human gene encoding and cartilage superficial
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; Murinae; Mus
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	IPSPIDTVFTRCNCEGKT 857	98 KPVDGLTTLRNGTLVAFRGHYFWMLNPFRPPSPPRRI	Db 7
	- 8	0 KPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRI	
	erven/GIIINEMESDETNICNG 949  :	39 EVNPDHEDADGGEGEKP-LIPGPPVLFPTAIPGTDLL	
		90 EVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPNMNVIDD	Qy 8
	- LEVMLPTTTIPKOTPNSKLV 889	82 KKPTSTKKPKT-PKTRKPKTTPAPLKTTSATPELNTTP-	
	9 6	KPTSTKKPKTMPRVRKPK	9 40
	KPQKPTKAPKPTKAP 829	27 ATTLAPKVTAP	
		79 TTTI,APKVTTTKKTTTTT	
	VTSTTTQDTTPFKITTLK 7		Db ×5
	PKEPGVPTTKTPAATKPEMTTTAKD 718	59 STPTTTKEPTTIHKSPDESTPELSAEPTPKALENS	
	EPEPTTPKKPEPTT 617	582 EPTTRKEPEPTTPKEPEPTTPKEPEPTP	Db !
	PKKPAPTTPETPPPTTSEV 658	KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPK	Qy
	PAPTTLKEPAPTTPKKP 5	APTTPKE	Qy
	   EPTTPKKP 54	515 KEPEPTIPKEPEPTTPKEPEPTTPKEP	Дb
	APTTPKKPAPKELAPTT 5	EPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAI	Qy
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	TTPEEPAPTTPKAAAPNTP 478	419 PTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTP	Qy
	512	핅-	Db
	KKPAPTAPKEPAPTTPKETA 418	PKEPAPTTPKKPAPTTPKEPAPTTT	Qy
	EPTTPKEPEPTTL 47	437 PEPTTTKEPESTTRKEPEPTTPKEP	Db
	APTTTKSAPTTPKEPSPTTT 358	APTTPKEPAPTTKEPSPTTE	Qy
	w	PTTPKEPEPTTPKEF	Db
	29	KKPAPTTPKEPAPTTPKE	Qy
	37	SKFLP	Db
	PAP 23	TTTKSAPTTPKEPAPTTKEPA	Qy
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	TPKEPTPTTIKSAPTT 1	APTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPK	Оу
	KKKTTSVKETRSAEKTS 31	255 VTPKPSLAPNSETSKEASLASNKETTVETKETTATNKQSSA-S	Дb
	KEKTTSAKETQSIEKTS 11	PRPSLPPNSDTSKETSLTVNKETTVETKETTTTN	Qy
		195 VKDNKKNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPPD	ДĎ
	KITTAKP	EAGSGLDNGDFKVT-	Qy
20;	11; Length 1054; 60; 36; Indels 368; Gaps	ry Match 44.2%; Score 2519; DB t Local Similarity 49.6%; Pred. No. 2.4e-1 ches 533; Conservative 38; Mismatches 1	Que Best Mato

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Best Local S
Matches 198
                                                                                                Q9N4S7 PRELIMINARY;
Q9N4S7;
Q9N4S7;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-JUN-2001 (TrEMBLrel. 17, L
Y51B11A.1 PROTEIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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SEQUENCE
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SEQUENCE FROM N.A.
TISSUE-ARTICULAR CARTILAGE;
Hughes C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Immunodetection and Partial Superficial Zone Protein, Syr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schumacher B.L., Hughes Aydelotte M.B.;
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
  Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1
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BL; AF056218; AAD13404.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-LPEAMLQTTTRPTPTPNSEIIDVNSENEDGDAAEGEKPHMIFRPPVLTPIVTPGTEII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 AA;
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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                                             Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ial cDNA Sequence of the Proteoglycan, Synthesized by Cells Lining Synovial
                        Caenorhabditis
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                                                                                                                      Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.3e-62;
0; Mismatches 37;
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                                                 Rhabditida;
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (WAR-2000) to the EMBL/Gen EMBL, AC006797; AAF60743.1; ".
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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STRAIN=BRISTOL N2;
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                                                   DKP-APTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPD
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Pred. No. 8.8e-57;
3; Mismatches 445
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rochas S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rochas S., Dlunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Gornes J., Dugar-Rochas S., Fleischmann W.,
RA Glodek A., Goong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodlra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nount S.M., Marshy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nount S.M., Marshy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nount S.M., Marshy B., Murphy L., Muzny D., Lai Z.,
RA Nount S.M., Marshy B., Murphy L., Muzny D.M., Nelson D.L.,
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NCBI_TaxID=7227;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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DR EMBL, AE003495, AAG22353.1.
DR Flybase, FBgn0030561, CG5228.
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TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTRTTAKPT
                             TSDKPAPTTPKE--TAPTTPKEPAPTTPKKPA---PTTPETPPPTTSEVSTPT-TTKEPT
                                                               EGTTAX----PTTLK----PTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTAKPTTLNPTEG
                                                                                              APTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK----KPAPKELAPTTTKGPTST
                                                                                                                              KPTTLKPTEGTSAQPTTLKPTEGTSAQSTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPT
                                                                                                                                                             K----KPA-----PKELAPT-----TTKEPTSTTSDKPA------PTTPKGT
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RX MEDINE-20196006; PubMed-10/3113;
RA Adams D.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D.D., Celniker S.E., Li P.W., Hookins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Horstin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Horstin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Menkolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Monnt S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Wang Z.-Y., Massarman D.A., Weinstook G.M., Weissenbach J.,
RA Wang Z.-Y., Massarman D.A., Weinstook G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rah Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rah Williams S.M., Woodage T., Weinstook G.M., Weissenbach J.,
Rah Yeiner R., Zaveri J.S., Zhan M., Zhang G., Zhang C., Zheng L.,
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EG:56G7.1 PROTEIN.
EG:56G7.1 OR CG14796.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE FROM N.A.

Cadieu E., Dreano S., Lelaure V., Mottier S., Galibert F.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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                               RTTPKVTTVIVSTQNPTTTTSKTSTVTI-----TTP-NPSPSTQRPTTTTRQPTSITAST
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                                                                                            PLTTLSTEEPNTTPKPLRTTTPTTTSVTATTRITTTISESSTETTSTOKPKSTTPTSTT
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096449;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYST GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRECURSOR.
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STRAIN-RACE 1-11;
Goernhardt B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ SEMBL; AF061185; AAC72308.1;
SEQUENCE 1489 AA; 164037 MW; 764CC79D1C2F5
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NCBI_TaxID=4787;
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Eukaryota; stramenopiles;
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es; Oomycetes; Pythiales; Py
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 853; DB 10;
Pred. No. 5.3e-49;
6; Mismatches 475;
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Q9SPMO;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
EXTENSIN-LIKE PROTEIN.
 TISSUE=POLLEN;
Stratford S., Barnes
Hohorst D., Gao M., (
                                                                 Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoideae; Andropogoneae; Zea.
                                            SEQUENCE FROM N.A.
                                                                                                                                         PEX2.
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3 W., Golubiewski A., Co
Showalter A., Bedinger
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InterPro; IPR001998; xylose_isom.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003952; LRR.out.
InterPro; IPR003592; LRR.out.
Pfam; PF00560; LRR; 3.
PFROSITE; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PXIOSE_ISOMERASE_1; UN
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UN
SMARF; SM00370; LRR; 3.
SEQUENCE 1315 AA; 134401 MW; 64C97A2
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                            TKPEMTTTAKDKTTERDLRTTP----ETTTAAPKMTKETATTTEKTTESKITATTTQVT 762
                                                                                                                    XKPLPPP----APVSSPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTL
                                                                                                                                                 TPKKPAPKELAPTTTKGPTSTTSDKPAPTT--PKETAPTTPK----EPAPTTPKKPAPTT
                                                            VSSPPPAPKSLPPPTPVSSP-----
                                                                                      PETPPPTTSEVSTPTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA
                                                                                                                                                                               PPAPVSSPPPTPKPLPPPAPVSSPPPVVKSSPPPTPVSSPPPTPKPLPPPPTPVSSPPPT
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Pred. No. 4.4e-46;
8; Mismatches 459
                                                                                                                                                                                                                                                                          -PTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson &
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Saunders D., Shownkeen
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Gootiquous nucleotide sequence from chromosome III of C
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NCBI_TaxID=6239;
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                                                            IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK------
                                                                                         KWKPVWDDDPDEPEADFTVPAPSKKPDTEDPADPLG-----
                                                                                                                                      TKPDSEAAADPVSGPTSKDPKLSKKAPVEKPKPTTDPKDDKLKPSPAKKPEKAPEPAAPK
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                                                                                                                                                             -PTTKTPAAT-----KPEMTTTAKDKTTERDLRTTPETT--TAAPK 737
                                        -----PKPKEVSKEPPKPTEPPKP-AAPKKWKPPWEDDPDEPE 1243
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DNA Res. 7:217-221(2000).
EMBL; AP001306; BAB03062.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1480 AA; 147153 MW; D1AC0C79F155E732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9LIE8
Q9LIE8;
01-OCT-2000
                                               562
                                                                                                    502
                                                                                                                              381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=COLUMBIA; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=COLUMBIA;
Kaneko T., Kato T.,
                                                                          429
                                                                                                                                                         445
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TPKEPAPTTPKEPAPTTPKETAP--TTPKGTAPTT---LKEPAPTTPKKPAPKELAPTTT
                                     TPPTATPPVAKPPVATPPIATPPTAKPPISTPPISKSPVATPPAATPPITTPPPAKPPVA
                                                               TPEKLAPTTPEKPAPTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNT---PKEPAPT
                                                                                                                    TPKEPAPTTPKEP--APTTTKKPAPTAP--KEPAPTTPKETAPTT-----PKKLTP--T
                                                                                           TPPLAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVATPPIAKPPVVTPPTT
                                                                                                                                                                         TTTKSAPTTTKEPAPTTTKSAPTTPKEP--SPTTTKEPAPTTPKEPAP---TTPKKPAPT
                                                                                                                                                                                                     VATPPTATSPIKTPPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPP
                                                                                                                                                                                                                        TTKEPAPTTP-KEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTT----KEPSPTTPKEPAP
                                                                                                                                                                                                                                                           PAKPPVAISPIVT---PPVTPIAOPPVATPPTATPPVATPPIATPPTSKSPISTPPISESP
                                                                                                                                                                                                                                                                                     PA-----PTTTKSAPTTP-KEPAPTTPKKPAP--TTPKEPAPTTPKEPTPTTPKEPAP
                                                                                                                                                                                                                                                                                                                PVAAPPITNPPISKPPVTTP----PTTTPPIAKPPIATPPISTPPAATPPAATPPITTLP
                                                                                                                                                                                                                                                                                                                                          KEPAPTTT----KSAPTTPKEPAPTTT-----KEPAPTTPKEPAPTTKE
                                                                                                                                                                                                                                                                                                                                                                      TQMPPIATP-PIAKSPVATPPIATPPTATPPITIPPVATPPITTPPIANPPIIMPPIATP
                                                                                                                                                                                                                                                                                                                                                                                                  SKV--LAKPTPKAETITKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                    KPPPSTPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 КРRРНРКРРNVK------РНРНРКРРТКРНРНРКРРТКННРНРКРРТІКРРРКРРSV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTS----PKITTAKPINPRPSL
                                                                                                                                                 -PPVAKPPVETPPIATPPTAKPPISTPPISKPPVATPPAATPPITTPTPVKPPVA
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29.6%; Pred. No. 1.7e-45;
Live 54; Mismatches 505
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EMBL/GenBank/DDBJ databases
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Best Local S
Matches 230
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Q41805; Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-JUN-2001 (TREMBLREL. 17, Last annotation update)
EXTENSIN-LIKE PROTEIN PRECURSOR.
Zea mays (Maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                      Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases. EMBL; Z34465; CAA84230.1; -. Mendel; 14346; Zeama; 2368; 14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-B73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                                      Mendel; 14346; Zeama;2368;14346.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 3.
SMART; SM00370; LRR; 4.
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                                                                                                  PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN
SDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 128
                                                                                                                                                                                                                                                                                      1188 AA;
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120980 MW; 2C77C7F8D7130149
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                                                        -DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ
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Mismatches
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220).
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                    Yotov W.V., St-Arnaud R.;
"Differential splicing-in of a proline-rich exon into a muscle-specific transcription factor.";
Genes Dev. 10:1763-1772(1996).
EMBL; U48364; AAB18734.1; -.
EMBL; U48363; AAB18732.1; -.
MGD; MGI:106095, Naca.
                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=96312450; PubMed=8698236;
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Sciurognathi; Muridae; Murinae; Mus
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QTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP----
                          DTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTK 827
                                                             T--SLAQTAPPSLQKAPSTTIPKENLAAPAV
                                                                                     TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ
                                                                                                                  KNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSIK-PVT 1611
                                                                                                                                             TSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA
                                                                                                                                                                           PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV 1554
                                                                                                                                                                                                       PKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP-----PPT 654
                                                                                                                                                                                                                                       VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A
                                                                                                                                                                                                                                                                  ----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKKPA 599
                                                                                                                                                                                                                                                                                                PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQT
                                                                                                                                                                                                                                                                                                                                                           KKTPKTAVPKETSAPSEGYTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP 1380
                                                                                                                                                                                                                                                                                                                                                                                                                      LTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP----SPQKIPKVAGPKEASATPPS
                                                                                                                                                                                                                                                                                                                                   PTTPKGTAPTTLKEPAPTTP--------
                                                                                                                                                                                                                                                                                                                                                                                        EPTPTT-----PEEPAPTTPKAAAPNTPKEPAPTTPKE-PAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPASKGVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKEPAPTTPKEPAPTTPKKPAPTT--PKE-----PAPTTPKEPAP-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGEISPSP 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK------EPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLEIPSAP 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT---PKEPAP----TTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE---TPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKSAPTTPKE-PAPTTTKSAPTTPK------EPAPTTTKEPAPTTPKEPAPTTTKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTSKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGP-PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPS----PQKTPKSVSLKGAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKE-----TSLTVNKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQSPKVDPIMSDVTPTSPKKTSATAV-PK-----DTSATLSLKSVPAVTSLSPPKAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·····-PKE-----PTPTTPKEPASTT-----PKEPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 776;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 003646AA864DEBFD CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
.1e-43;
                                                                                                                                                                                                                                                                                                                                ----KKPAPKELAPTTTKEPTS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 240;
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ACC DITION 
                                                                                                                  RESULT
Q9VEL9
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            FlyBase; FBgn0038492; CG4090.
InterPro; IPR002557; Chitin binding
InterPro; IPR000561; EGF-like.
Pfam; PF01607; Chitin_bind_2; 10.
SMART; SM00494; ChtBD2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan I.J., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Rasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG4090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
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13,
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Best Local Similarity
Matches 281; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHPDQIQTKPLKCKKVVSQGGSSSN-----STSNSSSSSNNSGSSSSNSGSSSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCGPGTVWDAQMQACNHAWAVKECGGIAPTTSTPTTSR-PTTASTSRPSDQTSTSRPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNNNQGSSSSSSSSSSSSSKPNPSETCKVNGQFIGDRSDCAKFYRCVDNDRGGFNMVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVRNNKGGFTSIPFQCGAGTVWDQDLQTCNHNFNNCSTGTESTTPKPPC--EPATNGTTA 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P----PTTARPVTARPTTSSPTTASSSQTTSPVTQAPNTDGKCRSEGFMADPNNCSKFYR
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                                                                                                                                                                                                                                                                                                                                                                                        PAEPITTTPSEESKDPGSTTPQSTDEPTTVTKPI-TKPTE-EPSTEKPQKPTTQYPEKPT
                                                                                                                                                                                                                                                                                                                                                                                                                  PKKPAPTTP----KEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt TECTGEGYMADPEDCRKYYRCINAGASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCSKL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITTSLPPTTTTGLPPTTTTGAQPTTTTLSSETETSTVTTSPESTTQPPSTTTMKPLPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTTKSAPTTPK---EPSPTTTKEPAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTSSTTTP--PPTTTDLPPTSTTGLP-PTTTTELPPT-----
                                                                                                                                                  GFFPDPEDCSRYYRCVDAAKNGKYQVYAFKCGKGTVWDTSTETCNYADQVSGN------
                                                                                                                                                                                                                                                                                                                              TTEE--PEKPOKPT-TTEYPOKPTTTEEPTPEKPOKPT-TTEYPOKPTTTEEPTPEKPOK
                                                                                                                                                                                                                                                                                                                                                 TPEKLAPTTPEKPAPTTPEELAPTTPEEPPTTTPEEPAPTTPKAAAPNTPKEPAPTTPKE
 TTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKA
                                                                                                                                                                              ---PAPKELA----PTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTP
                                                                                                                                                                                                            EPITTTT-LPSTTTDAIQEPTTSKKPEPTTTTESPESSTPEGSVTTLQPEPQPNYNCSSE
                                                                                                                                                                                                                          EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKK--
                                                                                                                                                                                                                                                                      PTTTEYPQKPTTEEPTTTSIPGYNPTTTSVPGYNPTTTPIPVETTTSTPGYK---PTTTG
                                                                                                                                                                                                                                                                                               PAPTT-PKEPAPTTPKETA-----PTTPK--GTAPTTLKEPAPTTRKKPAPKELAPTTTK 540
                                                         KPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQD
                                                                                                                     ETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAAT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TKEP----APT------TTKSAPTTPKEPAPTTPKKPAPTT
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nilarity 27.2%;
Conservative 9;
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                                  -SSPETTTT---VASETTTTTSGT
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Pred. No. 3e-41;
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                                                                                             ETTSKAPEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 316;
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                                       -TTTATPETTTKP 1895
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Zhang Y., Moreno C., Singh M.;
Zhang Y., Moreno M.;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROLINE-RICH MUCIN HOMOLOG.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria
Actinomycetales; Corynebacterineae; Mycobacteriaceae
NCBI_TaxID=1773;
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9; Mismatches 361
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## ALIGNMENTS

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SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,

Kelleher K. Giannotti J., Calvetti J., FitzGerald M., Kriz M.J.,

Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T.,

Bhatla S., Kriz R., Hewick R., Clark S.C.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U70136; AAB09089.1; -.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.

Ffam; PF01033; Somatomedin_B.

Pfam; PF01033; Somatomedin_B; 2.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Merberg D.M., Fitz L.J., Temple P., Glannotti FitzGerald M., Scaltreto J., Kelleher K., Prei Jacobs K., Turner K.;

(In) Preissner K.T., Rosenblatt S., Kost C., W Mosher D.F. (eds.);

Biology of vitronectins and their receptors., Elsevier Science Publishers B.V. (1993).
                                                                                                                                                                                                                                                                                                                                                                                                Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobbolz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.; Blacd 78:279-279(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEGAKARYOCYTE STIMULATING FACTOR.
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Eukaryota; Metazoa; C
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PROSITE; PS00024; HEMOPEXIN; UNKI
PROSITE; PS00524; SOMATOMEDIN_B;
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SEQUENCE 1404 AA; 151090 MW;
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Local Similarity 100.0%;
nes 1013; Conservative (
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                MPRYRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG
                        MPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG
 AEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRN
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Pred. No. 0;
0; Mismatches
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N_B; 2.
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Best Local Similarity 99.8
Matches 1011; Conservative
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Q9BX49;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR ).
BG174L6.2.
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EMBL; AL133553; CAC36090.
SEQUENCE 1404 AA; 1510
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                                                                                                  PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
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                                                                                              Query Match 42.4
Best Local Similarity 47.9
Matches 491; Conservative
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InterPro; IPR000285; Hemopexin.
InterPro; IPR0002965; P_rich_extensn.
InterPro; IPR001212; Somatomedin_B.
Pfam; PF01033; Somatomedin_B.
PRINTS; PR01021; PRICHEXTENSN.
PRINTS; PR01021; SOMATOMEDINB.
CMARPS. EMOROO22; SOMATOMEDINB.
                                                                                                                                                                                   SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOWATOMEDIN_B; 2.
SEQUENCE 1054 AA; 115991 MW; 4FC64B
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikegawa S., Nakamura Y.;
"a novel mouse gene highly homologous to a megakaryocyte stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRG4.

Mus musculus (Mouse).

Mus musculus (Mouse).

Theria; Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                        zone protein
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                  VKDNKKNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPDPPTTPHSKVATSPKTTAAKP
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                                                                                          Score 2294; DB 11;
Pred. No. 1.7e-141;
5; Mismatches 130;
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FFFK
                        FFFK 1013
                                          KPVDGLTTLRNGTLVAFRGHYFWMLNPFRPPSPPRRITEVWGIPSPIDTVFTRCNCEGKT
                                                      KPVDGLTTLRNGTLVAERGHYFWMLSPESPPSPARRITEVWGIPSPIDTVFTRCNCEGKT 1009
                                                                                         KKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLOTTTRPNOTPNSKLV
                                                                                                                                                                                             ATTLAPKVTAPAE----EIQNKPEETTPASEDSDDSKTTLKPQKPTKAPKPTKKPTKAP
                                                                                                                                                                                                             TTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKAT-----TPKP-QKPTKAP
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Best Local Similarity
Matches 294; Conserv
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Y51B11A.1 PROTEIN.
Y51B11A.1.
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01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cotton M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BRISTOL N2;
MEDLINE=99069613;
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STRAIN-BRISTOL N2;
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itted (MAR-1999)
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                    TPKAAAPNTPKEP--APTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTP
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TTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSS
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AAF60743.1; -.
2965; P_rich_extensn.
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Last annotation update)
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EMBL/GenBank/DDBJ
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Pred. No. 3.2e-55;
4; Mismatches 377;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.S.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Bealdwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berston K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Douck J., Brokstein P., Brottler P.,
RA Gebroy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebroy S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mcimtov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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CG5228.
CG5228.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Heretarygota; Neoptera; Endopterygota; Diptera;
Pterygota; Neoptera; Endopterygota; Diptera;
Pterygota; Neoptera; Endopterygota; Diptera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BERKELEY;
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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RT The genome sequence of Drosophila melanogaster.",
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DR Flybase; Fbgn030561; CG5228.
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TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTRTTAKPT
                              TSDKPAPTTPKE--TAPTTPKEPAPTTPKKPA---PTTPETPPPTTSEVSTPT-TTKEPT
                                                                EGTTAK --- PTTLK --- PTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTAKPTTLNPTEG
                                                                                               APTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK----KPAPKELAPTTTKGPTST
                                                                                                                                 KPTTLKPTEGTSAQPTTLKPTEGTSAQSTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPT
                                                                                                                                                                 K----KPA-----PKELAPT-----TTKEPTSTTSDKPA------PTTPKGT
                                                                                                                                                                                                   KGTTAKPTTLK---PTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTA
                                                                                                                                                                                                                                    TPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTA------PTTLKEPAPTTP
                                                                                                                                                                                                                                                                      TLKPTEGTTAKPTTLKPTKGTKGTSAKPTTLKPTEGTTAKPTTLKPTEGTTAKPTTLKPT
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                                                                                                                                                                                                                                                                                                                                       --PTTLKPTEGTTAK---PTTLK-PTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPT
                                                                                                                                                                                                                                                                                                                                                              PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPA---PTAPKEPAPTTPKETAPTT--PK 423
                                                                                                                                                                                                                                                                                                                                                                                                       TTAK---PTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAK- 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTEGTSAKPTTLKPTEGTSAKPTTLK--PTEGTTAKPTTLK--PTEGTSAKPTTLKPTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKET--QSIEKTSAK--DLAPTSKVLAKPT-----PKAETTTKGPALTTPKEPTPTT
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15; Mismatches 4
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RC STRAIN-BERKELEY;

RX MEDLINE-20196005; PubMed-10731132;

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N., Weinser D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.C., Pa
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
EG:56G7.1 PROTEIN.
EG:56G7.1 OR CG14796.
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Weinstock G.M., We Worley K.C., Wu D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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RTTPKVTTVIVSTQNPTTTTSKTSTVTI----
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYST GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRE
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Submitted (APR-1998) to the
EMBL; AF061185; AAC72308.1;
SEQUENCE 1489 AA; 164037
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Eukaryota; stramenopiles;
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Pred. No. 1.1e-47;
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TISSUE-ARTICULAR CARTILAGE; Schumacher B.L., Hughes C.E Aydelotte M.B.;
                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SUPERFICIAL ZONE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                              1403
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                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                      -----STKKP-KTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP--N
                                                                                                                                                                                                                                                                                                                                                                                                 TTYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPMEETPYE 1344
                                                                                                                                                                                                                                                                                                                                                                                                                    TTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAT---NSKATTPKP-QKPTKAPKKPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYAP----TEETTYEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEE 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTT------PFKITT---LKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTEET 1229
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               C.E.,
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            Kuettner
                                                                                              Ruminantia; Pecora; Bovoidea;
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          K.E.,
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Matches 255
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Best Local Similarity
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Q9SPMO;
O1-MAY-2000 (TrEMBLrel. 13, C:
O1-MAY-2000 (TrEMBLrel. 13, L:
O1-JUN-2001 (TrEMBLrel. 17, L:
O1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stratford S., Barnes W., Golubiewski A., Cotter R., Hohorst D., Gao M., Showalter A., Bedinger p.A.;

"Pollen Extensin-like (Pex) Genes in a Monocot and a Submitted (JUN-199) to the EMBL/GenBank/DDBJ datable EMBL; AR159297; AAD55980.1;

InterPro; IPR001611; LRR.

InterPro; IPR00198; xylose_isom.

InterPro; IPR001998; P_rich_extensn.
                                                                                                                                                                                                                                                          InterPro; IPR003592; LFR_out.
Pfam; PF00560; LRR; 3.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SMART; SM00370; LRR; 3.
SEQUENCE 1315 AA; 134401 MW; 64C97A2A01F0936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (mu.r.)
Eukaryota; Viridiplantae; Strept
Spermatophyta; Magnoliophyta; Li
Spermatophyta; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-POLLEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                  Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4577;
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
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J. Orthop. Res. 0:0-0(1998).
EMBL; AF056218; AAD13404.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000585; Hemopexin.

ofam. pr00045: hemopexin; 2.
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                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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401 AA;
                                                                                                  Conservative
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-KPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPR
                                                                                                                           14.98;
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yta; Liliopsida; Poales; Poaceae; PACC cl
                                                                                                  88;
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Last sequence update)
Last annotation update)
                                                                                   Score 808.5; DB 10,
Pred. No. 7.8e-45;
8; Mismatches 459;
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Pred. No. 1.1e
17; Mismatches
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                                                                                                                                                                                                                                                                  64C97A2A01F0936F CRC64;
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                                                                                                                                                     DB 10;
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                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a Dicot.";
                                                                                                                                                        Length
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                                                                                   219;
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		1303 K 1303	Db
		943 E 943	Qy
	1302	1272PKKEEDSTA	망
-	942	DMDYLPR	Qy
·	1271	ISSPPPAPVKPPSL	Db
	882	PKKPTSTKKPKTMPRVRKPKTTP	Qγ
	1228	1195 SPPPPAKSPPPPAPMSSLPPPVKSPPPPAPVSSP	Дb
	822	~	Qy
	1194	1147 SPPPELKSSPPPAPVSSPPSAPKSSPPPAPVSLPPPEVKSSPPPAPIS	ф
	762	PETTTAAPKMTKETATTTEKTTESKI	Qy
	1146	1097 VSSPPPAPKSLPPPTPVSSPPPEVKSSPPPTPVSSPPPAPKSSPPPTPVS	рь
	707	PTTSEVSTPTTTKEPTTIHKSPDES	Qy
	1096	1040 XKPLPPPAPVSSPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTL	Db
	647	594 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTT	Qy
	1039	980 PPAPVSSPPPTPKPLPPPAPVSSPPPVVKSSPPPTPVSSPPPTPKPLPPPPTPVSSPPPT	ф
	593	549 KPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT	Qy
	979	EKTSPPPATVSSPPF	망
	548	– SD	Qy
	922	863 SSPPLEPKPSSPPSSVSSPPTTVKSSPPPAPLSSPPMTPKSSSPPAHVSSPPEAEKSSPP	Db
	499	PAP 	Qy
	862	PV	DЪ
	439	LAPTTPE	Qy
	802	748PAPVSSPPPLKSSPPPVPESSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPP	Db
	379	KSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAP	Qy
	747	PPPSPVETLPPPSKSSPPEEPVSSPPQAPKSSSP	В
	319	PTT	Qy
	689	630 VASPPPPVKSPPPLAPVSSPSPPVKLPPLPAPGKSTPPPEEEKPTPPTPVKSSPPPEKSL (	DЪ
	259	PTTPKE-	ΩУ
	629	PMKSPPPPARVASPPPLMKSPPPPAPVASPPQPLKSPPPPVLWLSTPSVKSPPPPVP	Db
	210	PKEPTPTTIKSAPTTPKEPAPTTTKSAPTTP-KEPAPTTTKEPAPTTP	Qy
	571	512 SPPATPVKSSPPPAAVVLPPPAKTPSPPAPVASPPPEAPVSSPQPQVKSPPPPAPVASPP 5	Ф
	158	113 SIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE 1	Qy
	511	PPAAS	Db
	112	PSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQ	ΟV
	455	412 PTPGGPPSSSYPGKPPSVPGKPAAPAPMPTPHTPPDVSPEPL-PE 4	Db

RESULT Q20007

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Best Local :
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Q20007;
Q1-NOV-1996 (1
Q1-NOV-1996 (1
Q1-NOV-1998 (1
COSMID F35A5.
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Leimbach D.;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du 2., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Mortimore B., O'Callaghan M.,
Lightning J., Iloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
Netero 160: 2010.
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U46675; AAB52641.1; -
SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C1799F CRC64;
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STRAIN=BRISTOL N2;
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Submitted
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STRAIN-BRISTOL N2;
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513 TPVKNPVKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKP
                                                                                                                                                                                            454
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                                                                                                                                                                                                                                                                                                                                                                                                       SPYVPPTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNPTKKWKPPWEDETPVEEVKEPPVPEKKAPVLKKKDPAPAAKARDPSPSKAAPKKVEPS 333
                                                                                                                                                                                                                        KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP 199
                                                                                                                                                                                                                                                                                                  PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP 453
                                                                                                                                                                                                                                                                                                                                                    ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA-----
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                                                                                                                                                                                         EAPAKKTPVLKRKEPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPA- 512
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2e-44;
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                                                                                                                                                  -TTKSAPTTP 233
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RESULT
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C Q9LIE8; O7 01-0CT-2000 (TrEMBLrel. 15, Created)

T Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
T Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach-
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
C eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                Kaneko T., Kato T.,
Submitted (MAR-2000)
PubMed=10907853;
                                                SEQUENCE FROM N.A.
                                                                                                                                                      STRAIN-COLUMBIA;
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                                                                                           Nakamura Y., Asamizu E., T. EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  Embryophyta; Tracheoredons; core eudicots;
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                                                                                                                                                                                                                                                                                                    Tracheophyta;
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"Structural analysis of Arabidopsis thaliana chromosome sequence features of the regions of 4,251,695 bp covered TAC and BAC clones.";

DNA Res. 7:217-221(2000).

EMBL; AP001306; BAB03062.1;

InterPro; IPR002965; P_TiCh_extensn.

PRINTS; PR01217; PRICHEMSTENSN.

SEQUENCE 1480 AA; 147153 MW; D1AC0C79F155E732 CRC64.
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QDTTPEKITTLKTTTLAPKVTTTKKT----ITTTEIMNKPEETAKPKDRATNSKATTPKP
                                       TPPITTPPPAKPPVATPPIATPP---TAKPPVATPPTATPPIATSPVAKPPVAIPPIKTPP
                                                                 TKPEMT-TTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT
                                                                                                              TPPPTTSEVSTPTTTKEPTTIH--KSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA
                                                                                           TPPIAKPPVATPPTTAPPTATPPVAKPPVATPPIATPPTAKPPILTPPISKPPVATPPAA
                                                                                                                                               MPPIATPPTAKPPIATPPIAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVA
                                                                                                                                                                          APKELAPTTTKGPTST--TSDKPAPTTPKETAPT-TPKEPAPTTPKKPAPTTP----E
                                                                                                                                                                                                     KPPVAT---PPTATPPIATPPIATPPVVTPPTATPPVATPPIAKPPTTI--PPTATPPVA
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                                                                                                                                                                                                                                                         TPPIATPPIAKPPVATPPTATPPIATSPVAKPPVATPPIKTPPPAKPPVAIPPIATPPVA
                                                                                                                                                                                                                                                                                   TPKEPAPTTPKEPAPTTPKETAP---TTPKGTAPTT----LKEPAPTTPKKPAPKELAPTTT
                                                                                                                                                                                                                                                                                                              TPPTATPPVAKPPVATPPIATPPTAKPPISTPPISKSPVATPPAATPPITTPPPAKPPVA
                                                                                                                                                                                                                                                                                                                                        TPEKLAPTTPEKPAPTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNT----PKEPAPT
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTENSIN-LIKE PROTEIN PRECURSOR.
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; Liliopsida; Poaceae; PACC cl
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendel; 14346; Zeama; 2368; 14346.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=B73; TISSUE=POLLEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panicoideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPPVTNPPTAMPPIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLPPIAKPPVETSPTATPPTATPPVAIPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AMLQTTTRPNQTPNSKL--VEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLPRVPNQGIIINPMLS
                                                                                                                                                                                                                                                                                                              PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN 68
                                                                                                                                                                                                                                                                                       PTPHSPPAD------DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ 510
                                                                                                      PKKPAPTTPKEPAPTT-----PKE----PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKP
                                                                                                                                                                                                          -----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPA
                                                                                                                                                                                                                                                          SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTSAKETQSIEKTSAKDLAPTSKV 128
 EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTTKKPAPTAPKEPAP
                           SP--PKEPVSSPPOTP----KSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSP----
                                                  APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK
                                                                              PAKSTPPPEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPPQEKPTPPSTPSKP-PSSPEKP
                                                                                                                                PPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPPMKSPPPPTPVSSPPPPEKSPPPPP
                                                                                                                                                         PTTTKSAPTTP--KEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP-KEPAPTT
                                                                                                                                                                                   SPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPPVKSP--PPPTLVASPPPPVKSPP
                                                                                                                                                                                                                                                                                                                                           230;
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MW; 2C77C7F8D7130149
                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.80
); Mismatches
                                                                                                                                                                                                                                                                                                                                                          Score 784; DB 10;
Pred. No. 2.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                          -SPPPPVKTTSPPAPIG----SPSPPPPVSVV
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                                                                                                                                                                                                                                                                                                                                                 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VVKPPVAIPPITKPPV
                                                                                                                                                                                                                                                                                                                                                                       Length 1188;
                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local S
Matches 288
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1116
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                                                                                                                                                                                                                                                                                                                                                                              Pfam; PFC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into a muscle-specific transcription Genes Dev. 10:1763-1772(1996).
EMBL; U48364; AAB18734.1; -.
EMBL; U48363; AAB18732.1; -.
MGD; MGI:105095; Naca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINB=96312450; PubMed=8698236;
YOtoV W.V., St-Arnaud R.;
"Differential splicing-in of a proline-rich
"Differential splicing-in tanscription factor.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002715; NAC.
InterPro; IPR003037; TS-N.
Pfam; PF01849; NAC: 1.
Pfam; PF02094; TS-N; 1.
Pfam; PF02094; TS-N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NACA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKE---PA----PTTPKK----PAPKELAPTTTKE---PTSTTSDKPAPTTPKGTAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTTVISP-PSEPKSSPPPTPVSLPPPIVKSSPPPAMVSSP-PMTPKSSPPPVVVSSPPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET
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                                                                                                                                                                                                VTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKE------TSLTVNKETT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPPPAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL
                                                                                                                                                         VQSPKVDPIMSDVTPTSPKKTSATAV-PK-----DTSATLSLKSVPAVTSLSPPKAPV
          LTT---
                                                         APSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPS----PQKTPKSVSLKGAPA
                                                                                                     VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 144
                                                                                                                                                                                                                                                              288;
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                        2187 AA;
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                                                                                                                                                                                                                                                              Conservative
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Rodentia;
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220599
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27.7%;
               PKE-----
                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                 Score 776; DB 11;
pred. No. 1.6e-42;
2; Mismatches 389;
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Sciurognathi;
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                  -PTPTTPKEPASTT--
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thi; Muridae;
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                            PKEPTPTT
                                                                                                                                                                                                                                                                           240;
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                   O9VEL9;

01-MAY-2000 (TrEMBLrel. 1

01-MAY-2000 (TrEMBLrel. 1

01-JUN-2001 (TrEMBLrel. 1

CG4090 PROTEIN.
Drosophila melanogaster (Fruit fly)
                                                                                                         Q9VEL9
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                                                                                                                                                                           1753 DSHISPVS-DACSTGTTTP 1770
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                                                                                                                                                                                                                                                                                                                                          T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP
                                                                                                                                                                                                                                                      APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK
                                                                                                                                                                                                                                                                                                              DTTPFKITTLKTTTLAPKYTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTK
                                                                                                                                                                                                                                                                                                                                                                       TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ
                                                                                                                                                                                                                                                                                                                                                                                                    KNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSIK-PVT
                                                                                                                                                                                                                                                                                                                                                                                                                      TSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKKPA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP 1380
                                                                                                                                                                                                                                     -PKKASSSKRASTLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTTPKGTAPTTLKEPAPTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPTPTT-----PEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP----SPOKIPKVAGPKEASATPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPASKGVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKEPAPTTPKEPAPTTPKKPAPTT--PKE-------PAPTTPKEPAP------T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGEISPSP 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK-----EPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLEIPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE---TPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKSAPTTPKE-PAPTTTKSAPTTPK------EPAPTTTKEPAPTTPKEPAPTTTKEP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLETPPCSKKAPKTAAPKESSATSSSKR 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTSKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGP-PAT
                                                                                                      PRELIMINARY;
                                            13,
13,
                                       Created)
Last sequence update)
Last annotation updat
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                                          update)
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RA Adams M.D., Cschiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Cschiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Cschiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Cschiker S.E., Kichards R.A., Gocayne J.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burdion R.C., Rogers Y.-H.C., Blazej R.G., Champe M. Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Bortis K.C., Blazej R.G., Charper H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Heurst M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Heurst M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattel B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Liako P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Merkulov G., Milshinan N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Williams S.M., Moodage T., Wortley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Massaman D.A., Weinstock G.M., Weissenbach J.,
Ra Wang Z.-Y., Massaman D.A., Weinstock G.M., Veissenbach J.,
Rhen Globs R.A., Shyrs B.W., Jahn M., Jahng G., Zhao Q., Zheng L.,
Rhen J., Shan M., Jahna M., Jahna W., Shao Q., Zheng L.,
Rhen J., Shan M., Shao G., Shan M., Shao Q., Zh
                                                                                                                                                                                                                                                                                 Matches
                     1131 NNNNQGSSSSSSSSSSSSTSSKPNPSETCKVNGQFIGDRSDCAKFYRCVDNDRGGFNMVPF
                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0038492; CG4090.
InterPro; IPR002557; Chittin_binding.
InterPro; IPR000551; EGF-like.
Pfam; PF01607; Chittin_bind_2; 10.
SMART; SM00494; ChtBD2; 11.
144
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                         4 NKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRP
                                                                                                                                                                                                                                                                                                  Local
                                                                                                   SSSSNSGSSSNTGSSSNSGASSSGGSSNQGSSSNSGSSSGSNSSGNQSTSSSTSSSSSSS 1130
                                                                                                                                            SLPPNSDTSKETSLTVNKETTV---ETKETTTTNKQTS----TDGKEKTTSAKETQSI--
                                                                                                                                                                                  NHPDQIQTKPLKCKKYVSQGGSSSN-----STSNSSSSSNNSGSSSSNSGSSSS-----
                                                                                                                                                                                                                                                                                 281;
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                              2112 AA;
                                                                                                                                                                                                                                                                             Conservative
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A; 219547 MW;
                                                                                                                                                                                                                                                                                            13.6%;
                                                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                                                                                          Score 739;
Pred. No. 4
                                                                                                                                                                                                                                                                  Pred. No. 4e-4
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       B91018E5551A5D36 CRC64;
                                                                                                                                                                                                                                                                                          4e-40;
                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                         Length 2112;
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                Gaps
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O9XDH2
PREMERTEL 12, Created)
01-NOV-1999 (TrEMBERTEL 12, Last sequence update)
01-NOV-1999 (TrEMBERTEL 17, Last sequence update)
01-JUN-2001 (TrEMBERTEL 17, Last annotation update)
PROLINE-RICH MUCIN HOMOLOG.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Mycobacterium.
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Zhang Y., Moreno C., Singh M.;
"Cloning and characterization of a new member of the PGRS family 1
is a useful marker of polymorphism in Mycobacterium tuberculosis.'
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR071081; AAD01594.1; .
InterPro; IPR002951; Atrophin
InterPro; IPR002955; P_rich_extensn.
InterPro; IPR003882; Pistil_extensin.
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Q91ie8 arabidopsis
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Q91]64 arabidopsis	077765 bos taurus	Q9sbml volvox cart	Qynkcy drosophila		-	٦,								ດ	w	023587 caenorhabdi	017362 caenorhabdi	09zq10 arabidopsis	010465 homo sapien	7	homo out		תכ	_		094185 Caenorhahdi

## ALIGNMENTS

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Merberg D.M., Fitz L.J., Temple P., Giannotti J.,

FitzGerald M., Scaltreto J., Kelleher K., Preissn

Jacobs K., Turner K.;

L (In) Preissner K.T., Rosenblatt S., Kost C., Wege

L Mosher D.F. (eds.);

Biology of vitronectins and their receptors., pp

L Biology of vitronectins and their receptors., pp
Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U70136; AAB09089.1; -

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR002400; GF_cysknot.
Pfam; PF003; Somatomedin_B.

Pfam; PF0103; Somatomedin_B; 2.
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Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Turner K.J., Fitz L.J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.;

Blood 78:279-279(1991).
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Q92954;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEGAKARYOCYTE STIMULATING FACTOR.
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PROSTTE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
SMART; SM00201; SO; 2.
SEQUENCE 1404 AA; 151090 MW; AABD7A
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                                                                                                  KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
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{\tt AEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRN
            MPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGG
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O9BX49; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BG17416.2: (MSF: MEGAKARYOCYTE STIMULATING FACTOR ).
BG17416.2.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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REMBL: AB034730; BAA92310.1; -.

RMGD; MGI:18911344; Pr94.

RINterPro; IPR000585; Hemopexin.

R InterPro; IPR0002965; P_rich_extensn.

R InterPro; IPR001212; Somatomedin_B.

R InterPro; IPR001212; Somatomedin_B.

R Pfam; PF01033; Somatomedin_B, 2.

R PRINTS; PR01217; PRTCHEXYENSN.

R PRINTS; PR00127; PRTCHEXYENSN.

R PRINTS; PR0022; SOMATOMEDINB.

R SMARR; SM00210; SO; 2.

R SMARR; SM00201; SO; 2.

R PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.

R PROSITE; PS00024; SOMATOMEDIN_B; 2.

SEQUENCE 1054 AA; 115991 MW; 4FC64BFA4228323
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Q9JM99;
Q1-Q2T-2000 (TrembLrel. 15, Created)
Q1-QCT-2000 (TrembLrel. 15, Last sequence update)
Q1-JUN-2001 (TrembLrel. 17, Last annotation update)
MRNA, COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING
PRECURSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
                                                                                                                                                                                    Ikegawa S., Nakamura Y.;
"a novel mouse gene highly homologous to a megakaryocyte stimulating factor precursor
                                                                                                                                                                                   zone protein
                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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VKDNKKNTPKKKPNPEPPAVDEAGSGLONGEFKLTPPPPDPPTTPHSKVATSPKTTAAKP
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                               ; Score 2046; DB 11;
; Pred. No. 3.1e-123;
34; Mismatches 128;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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and cartilage
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                                                                KPVDGLTTLRNGTLVAFRG
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RESULT
Q9N4S7
ID Q9
AC Q9
DT 01
DT 01
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DT V5
Q9N4S7 PRELIMINARY;
Q9N4S7;
01-OCT-2000 (TrEMBLrel. 15, 0
01-OCT-2000 (TrEMBLrel. 15, 1
01-JUN-2001 (TrEMBLrel. 17, 1
Y51B11A.1 PROTEIN.
                                                                                                                                                   KPVDGLTTLRNGTLVAFRG
                                                                                                                                                                                                                                        EVNPDHEDADGGEGEKP-LIPGPPVLFPTAIPGTDLLAGRLNRGININPMPSDETNLCNG
                                                                                                                                                                                                     EVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNG
                                                                                                                                                                                                                                                                                              ATTLAPKVTAPAE-----EIQNKPEETTPASEDSDDSKTTLKPQKPTKAPKPTKKPTKAP
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STRAIN-BRISTOL N2;
MEDLINE-99069613;
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y51B11A.1.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology. The C Science 282:2012-2018(1998).
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STRAIN-BRISTOL N2;
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                      KKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTTPKEPAPTTPKEP--APTTPKGTA
                                               TTTTAPETTSTEPPSSSTTPVQTTTTTAPETTSTEPPSSS-TTPVQTTTTTAPETTSTEP
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EMBL/GenBank/DDBJ
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Mandri D., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Cawley S., Dahlke C., Davems-P., Harder P., Brottier P., Brottier P., Rottier P., Brottier P., Brottier P., Center A., Chandra I., E., Garg N.S., Gelbart P., Brottier A., Chandra I., Dew J., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Harris N.L., Harvisky A.A., Li J., Li Z., Kennison J.A., Ketchum K.A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q917S1;
01-MAR-2001
01-MAR-2001
01-JUN-2001
CG5228 PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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EMBL, ABD03495; AA022353.1; -. ENBLO3495; AA022353.1; -. ENBLO3495; BA022353.1; -. ENBLO3495; BA02335.1; -. ENBLO3495; AA022353.1; -. ENBLO3495; AA0
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TL--KPTEGT----SAKPTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPTERTSAQPTTLK
                                              TIHKSPDESTPELSAEPTP------KALENSPKEPGV--PTTKT---PAATK
                                                                                              TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTRTTAKPT
                                                                                                                                          TSDKPAPTTPKE--TAPTTPKEPAPTTPKKPA---PTTPETPPPTTSEVSTPT-TTKEPT
                                                                                                                                                                                                                                         APTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK----KPAPKELAPTTTKGPTST
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RX MEDLING-2019606; pubMed=10731132;
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen M., Miklos G.L.G., RA RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Gle Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., RA Harris N.J., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.J., Houtsh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Llang Y., Lin X., Liu X., wattei B., McIntosh T.C., McLeod M.P., Mcherson D.L., RA McInton D.R., Nelson K.A., Nixon K., Nuxskern D.R., Moshrefi A., Palataxolo M., Pittman G.S., Pan S., Pollard J., Purl V., Resse M.G., RA McInton S.M., My M., Murphy B., Murphy L., Murpy D., McC., Scheeler F., Shen H., Mang X., Mang X., Mang X., Ma
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01-NOV-1999 (TrEMBLrel. 12, Last seque
01-JUN-2001 (TrEMBLrel. 17, Last annoted)
EG:56G7.1 PROTEIN.
EG:56G7.1 OR CG14796.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Trachelterygota: Metazoa; Endopterygota: Drosophila melanogaster.
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soptera; Endopterygota; Diptera; Brachycera; Musc
Drosophilidae; Drosophila.
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EMBL; AL031028; CAA19845.2; -.
FlyBase; FBgn0025390; EG:5667.1.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; Chitin_bind_2; 2.
PRINTS; PR001217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10
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[2]
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Cadieu E., Dreano S., Lelaure V., Mottier S., Galibert F.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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TSIGTTRIPTTTNPQNSTSSTDLTTVTRPPCPDPDSTSDKNTNTACTQELQQVNLLELQS
                        PAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTT-TKE-----
                                                                               PTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP-TTTKGPTSTTSDK
                                                                                                         PLTTLSTEEPNTTPKPLRTTPTTTTSVTATTRITTTTISESSTETTSTQKPKSTTPTSTT
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                                                                                                                                                              TSSTQRATSTTSEPTKTT-QNITTTTPKPTTLKTSTQEATTSTQKVSTVTITTKKATESS
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No. 1.4e-47;
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Phytophthora infestans (Potato late blight fungus)
Eukaryota; stramenopiles; Oomycetes; Pythiales; Py
Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF061185; AAC72308.1; .. SEQUENCE 1489 AA; 164037 MW; 764CC79D1C2F5163 CRC64
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AY-1999 (TrEMBLrel. 10, Last sequence update)
AY-1999 (TrEMBLrel. 10, Last annotation update)
GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRE
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Q9SPMO;
O1-MAY-2000 (TrEMBLrel. 13, 0
O1-MAY-2000 (TrEMBLrel. 13, 1
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EXTENSIN-LIKE PROTEIN.
                                                                                                                                                                                                               Zen mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
Stratford S., Barnes W., Golubiewski A., Cotter R., McC Hohorst D., Gao M., Showalter A., Bedinger P.A.; "Pollen Extensin-like (Pex) Genes in a Monocot and a Di Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF159297; AAD55980.1; -.
                                                                                                                                     TISSUE-POLLEN;
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InterPro; IPR001998; xylose_isom.
InterPro; IPR002995; p_rich_extensn.
InterPro; IPR003599; LRR_out.
Pfam; PF00560; LRR; 3.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SMART; SM00370; LRR; 3.
SECHEMPTE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Sinhes 255;
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STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKP
                                                           TKPEMTTTAKDKTTERDLRTTP----
                                                                                        VSSPPPAPKSLPPPTPVSSP-
                                                                                                                                      XKPLPPP----APVSSPPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTL
                                                                                                                                                                 TPKKPAPKELAPTTTKGPTSTTSDKPAPTT---PKETAPTTPK----EPAPTTPKKPAPTT
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                                                                                                                                                                                                                                                                                                        SSPPLEPKPSSPPSSVSSPPTTVKSSPPPAPLSSPPMTPKSSSPPAHVSSPPEAEKSSPP
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Pred. No. 4.6e-44
B; Mismatches 45
                                                                                  ----PPEVKSSPPPTPVSSPPPAPKSSPPPTPVS
                                                      ETTTAAPKMTKETATTTEKTTESKITATTTQVT
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Q20007;
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 08, Last sequence updi
Q1-NOV-1998 (TrEMBLrel. 08, Last annotation updi
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Ravello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Filoyd C., Mcmurray A., Saunders D., Shownkeen I
Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases EMBL; U46675; AAB52641.1; -. SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C1799F CRC64
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STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APAAVKKPEPISKPKDTAPKKAEPNSPVVP-PTPVKNPVKKWKPPWEDDDAPAKPVSLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWKPVWDDDPDEPEADFTVPAPSKKPDTEDPADPLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK-PDPKIPEV-PPTPVKNPVKKWKPPWEDDDEPSEPVSAPEPEKKTPVLAKKAPTKPA 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSA-EP---TPKALENSPKEPG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTPVKNPVKKWKPPWEDDDEPAEPVSAPEPEKKTPVLAKKAPAKPRDP----SPKKAAPV 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APTITKGPTS-----TTSDKP-----APTIPKET-----APTIPKEPAPTIPKKPAPT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-KEPEKPKD-APKVAAKPRDPSPKKAVPE--KEPAKVAAKPRDLSPKKAIPIPANTQEA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT-----TPKKPAP-----KEL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSPKKAEPNSPVVP----PTPVKNPVKKW-KPPWEDDDEPTEEVKKPSE--PEKKTPVLA
                                                                                                                                                                                                                                                                                                                                                                                                IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK---
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                                                                                                                                                                                                                                                                        ---TTPTPRKMTSTMP
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                                                                                                                                                                                                                 ADFTMPAPKKPDTEDP
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(TrEMBLrel. 15, PRELIMINARY;

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Best Local
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01-JUN-2001 (TremBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:217-221(2000).
EMBL; AP001306; BAB03062.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1480 AA; 147153 MW; D1A
        540
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"Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 4,251,695 bp covered TAC and BAC clones.";
                                   622
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PubMed-10907853;
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Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                                                                                                                                             126
                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTS----PKITTAKPINPRPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
KEPTSTTSDKPAPTTPKGTAP-TTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKP
                         TPPIATPPIAKPPVATPPTATPPIATSPVAKPPVATPPIKTPPPAKPPVAIPPIATPPVA
                                                   TPKEPAPTTPKEPAPTTPKETAP--TTPKGTAPTT---LKEPAPTTPKKPAPKELAPTTT
                                                                              TPPTATPPVAKPPVATPPTATPPTAKPPISTPPISKSPVATPPAATPPITTPPPAKPPVA
                                                                                                        TPEKLAPTTPEKPAPTTPEELAPTT-PEEPTPTTPEEPAPTTPKAAAPNT----PKEPAPT
                                                                                                                                    TPPLAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVATPPIAKPPVVTPPTT
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                                                                                                                                                                                                                 TTTKSAPTTTKEPAPTTTKSAPTTPKEP---SPTTTKEPAPTTPKEPAP----TTPKKPAPT
                                                                                                                                                                                                                                            VATPPTATSPIKTPPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPP
                                                                                                                                                                                                                                                                     TTKEPAPTTP-KEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTT----KEPSPTTPKEPAP 325
                                                                                                                                                                                                                                                                                                PAKPPVAISPIVT--PPVTPIAQPPVATPPTATPPVATPPIATPPTSKSPISTPPISESP
                                                                                                                                                                                                                                                                                                                          PA-----PTTTKSAPTTP-KEPAPTTPKKPAP--TTPKEPAPTTPKEPTPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                     PVAAPPITNPPISKPPVTTP----PTTTPPIAKPPIATPPISTPPAATPPAATPPITTLP
                                                                                                                                                                                                                                                                                                                                                                               KEPAPTTT----KSAPTTPKEPAPTTT-----KEPAPTTPKEPAPTTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                   SKV--LAKPTPKAETTTKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTP 179
                                                                                                                                                                                                                                                                                                                                                                                                         TQMPPIATP-PIAKSPVATPPIATPPITATPPITIPPVATPPITTPPIANPPIIMPPIATP
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bred. No. 1.7e-43;
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EMBL/GenBank/DDBJ databases
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RESULT Q41805
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Best Local (
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SIGNAL
SEQUENCE
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Q41805;
Q41805;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTENSIN-LIKE PROTEIN PRECURSOR.
Zea mays (Maize).
Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cla
          511 APVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-B73; TISSUE-POLLEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                      PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN 68
                                         SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 128
                                                                                                         PTPHSPPAD-
                                                                                                                                                                                                      230;
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                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                              POTENTIAL. MW; 2C77C7F8D7130149 CRC64;
                                                                                                                                                                                                                        Score 784;
Pred. No. 1
                                                                                                                                                                                               Mismatches
SPPPPVKTTSPPAPIG----SPSPPPPVSVV
                                                                                                                                                                       DB 1.5e-42;
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                                                                                                                                                                                                                                          Length 1188;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
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                                                                                                                                                                Yotov W.V., St-Arnaud R.;
"Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle-specific transcription factor.";
Genes Dev. 10:1763-1772(1996).
EMBL; U48364; AAB18734.1; -:
InterPro; IPR002715; NAC.
InterPro; IPR003037; TS-N.
Pfam; PF01849; NAC; 1.
Pfam; PF02094; TS-N; 1.
                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96312450; PubMed=8698236;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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                                                                                                             U48364; AA
U48363; AA
MGI:106095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 27.7%; Phes 288; Conservative 122;
                                                                                                                                                                                                                                                                                                                                                              507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPS----PQKTPKSVSLKGAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQSPKVDPIMSDVTPTSPKKTSATAV-PK-----DTSATLSLKSVPAVTSLSPPKAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKSAPTTPKE-PAPTTTKSAPTTPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTSKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGP-PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VETKETTTINKOTSTDGKEKTTSAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGVTAVPPEISLPPKETPONATPNESLAASSOKRSPKTSVPKETPPGGVTAMPLEIPSAP 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKR
                                                                                                                                                                                                                                                                                                                                                                                       KKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGEISPSP 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK------EPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE---TPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APTT--TKSAPT------
                                                                                                                                                                                                                                                                         VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A 1496
                                                                                                                                                                                                                                                                                                                                 PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                               LTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP-----SPQKIPKVAGPKEASATPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKEPAPTTPKEPAPTTPKKPAPTT--PKE-----PAPTTPKEPAP-----T
APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK 887
                                                                                                  T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP 1665
                                                                                                                     TKPEMITTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ
                                                                                                                                                         TSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA 707
                                                                                                                                                                                                                PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV 1554
                                                                                                                                                                                                                                        PKELAPITIKGPTSITSDKPAPTIPKETAPTIPKEPAPTIPKKPAPTIPETP-----PPT
                                                                                                                                                                                                                                                                                          ----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKKPA
                                                                                                                                                                                                                                                                                                                                                            PTTPKGTAPTTLKEPAPTTP----
                                          QTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP-----
                                                                     DTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPKPQKPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                         -PEEPAPTTPKAAAANTPKÉPAPTTPKE-PAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PKE-----PTPTTPKEPASTT-----PKEPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220599 MW; 003646AA864DEBFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 776; DB Pred. No. 8.6e-22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKEPAPTTPKK-PAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EPAPTTTKEPAPTTPKEPAPTTTKEP
                                                                                                                                                                                                                                                                                                                                                                 -----KKPAPKELAPTTTKEPTS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 240;
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RESULT OPVELY OF THE CONTROL OF THE 
                                                                   RX MEDLINE-20156005; pubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Handerson S.N.,
RA Berondon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Baridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Boliskov S.
RA Borkova D., Botchan M.R., Bouck J., Harts C., Charter A., Chandra I.,
RA Cherry J.M., Cawley S., Dehlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dehlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Collect C., Gabrielian A.E., Garg M.S., Gelbart W.M., Classer K.,
RA Clodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg M.S., Gelbart W.M., Classer K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.R.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kulman M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Kulman M., Kalush F., Karpen G.H., Kaz, M.R., Shen H.,
RA Kulman M., Kalush F., Karpen G.H., Kaz, M.R., Shen H.,
RA Kulman M., Kalush F., Karpen G.H., Kaz, M.R., Shen H.,
RA Kulman M., Kalush F., Karpen G., Scheler F., Shen 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG4090 PROTEIN.
CG4090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1717 -PKKASSSKRASTLP------ATTLPSLKEASVLS------PTATSSGK 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888 LVEVNPKSEDAGGAEGETP 906
                                   2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                   ξ
; EGF_1; 1.
AA; 219547 MW;
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                 B91018E5551A5D36 CRC64;
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		PKKPTSTKKPKTMP 842	829	Qy
	9	TNTSA	1896	Дδ
	828	KVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKA	769	Оy
	8	111: TTTKP	1858	Db
	σ	EMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQD	709	Qy
	1857	ETTSKAPENTTTWA	1817	Db
	90	TSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAAT	649	Qy
	മ	: : :	1764	Db
	<b>D</b>	PKEPAPTTOKKDADTTO	598	γQ
	1763		0	Db
	1	EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKE-DADTTDKE-DADTTDKCTADTTTKCTADTTTKCT	541	Qy
	540	FATET TO REAPTIVE STATE OF A PITEK PITEK - GTARTITEK PAPTITEK PAPKELAPTITK	1648	D 43
	1647	TTEEPEKPQKPT-TTEYPQKPTTTEEPTPEKPQKPT-TTEYPQKPTTTEEPTPEKPQK	o G	25
	488	TPEKLAPTTPEEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTP	, 2	Qy
	G	PAEPITTTPSEESKDPGSTTPQSTDEPTTVTKPI-TKPTE-EPSTEKPQKPTTQYPEKP	1534	В
	N	PKKPAPTTPKEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLT	374	Qy
	1533	TECTGEGYMADPEDCRKYYRCINAGASYRKYNFTCPKGTGWNEEVQTCDYVENIPRCS	1474	Db
	373		364	Qy
	14	TTTTSLPPTTTTGLPPTTTTGAQPTTTTLSSETETSTVTTSPESTT	1414	Db
	363	PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK	309	Qγ
	1413	TSTSSTITPPPTTTDLPPTSTTGLP-PTTTTELPPTTTTDLPPTTTTRLP	1364	Дb
	9	PAPTTPKEP	249	Qy
	1363	GTVWDQDLQTCNHNFNNCSTGTESTTPKPPCEPATNGTT	130	Db
	o c	APTPTKSAPTTPKEDAPTTPKKDAPTTPKKDAPT	21	Оу
	1305	DGKCRSE	125	Db
	217	TPKEPAPTTTKEPAPTTPKEPAPTT	17	Qy
	<u> </u>	:  :   ASTSRPSDOT	119	рь
	78	4ALTTPKEPTPTTPKEPASTTPKEPTPTTPKEPASTTPKEPTPTTTKSAPT	14	у
	1190	1 NNNNQGSSSSSSSSSSTSSKPNP	113	Db
	143	EKTSAKDLAPTSKVLAKPTPKAETTTKGP	115	Qy
	-	SSSSNGGSSNTGSSSNGGSSSNGGSSSNGGSSSSGSNSGNSGNSSTSSSTS	107	Db
	114	SLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETOSI-	64	Оу
	ь ,	NHPDQIQTKPLKCKKVVSQGGSSSN:  :: :::   :  ::	102	DЬ
	ר עכ	SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRP		Оу
44.	809	atch 14.3%; Score 739; DB 5; Length 2112; cal Similarity 27.2%; Pred. No. 1.9e-39; 281; Conservative 98; Mismatches 339; Indels 316; G	Query M Best Lo Matches	

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1929

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Laclette J.L., Mondragon-Palomino M., Martens A.,

Zhang Y., Moreno C., Singh M.;

"Cloning and characterization of a new member of the PGRS family that

"sa useful marker of polymorphism in Mycobacterium tuberculosis.";

"Is a useful marker of polymorphism in Mycobacterium tuberculosis.";

"Is submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

"EMBL; AF071081; AADA1594.1; -.

"REMBL; AF071081; AATophin.

"InterPro; IPR002951; Atrophin.

"InterPro; IPR002955; Parich_extensn.

"InterPro; IPR002955; Parich_extensn.

"InterPro; IPR003882; Pistil_extensin.

"PRINTS; PR01217; PRTCHEXTENSIN.

"PRINTS; PR01217; PRTCHEXTENSIN.

"PRINTS; PR01218; PSTLEXTENSIN.

"PRINTS; PR01218; PSTLEXTENSIN.

"PRINTS; PR01218; PSTLEXTENSIN.

"PRINTS; PR01218; PSTLEXTENSIN.
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Best Local Similarity
Matches 248; Conserv
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Q9XDH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TREMBLrel. 12, 01-NOV-1999 (TREMBLrel. 12, 01-JUN-2001 (TREMBLREL. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROLINE-RICH MUCIN HOMOLOG. Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 PTPKAETTIKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTIKSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                    484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 251
                                                                                                                                                                                                                                                                                                        TTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAP ----TTTKKPAPTAPKEPAPTTPKETAP
                                                                                                                                                                                                                                                                                                                                                                                                             SRPALPPCPPPPVVIPDPPEPAAPPVPPAPNSPPFPPFPPAPKFVPAPPVP---PVPNSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPTTPKEPTPTT----PKEPAPTTKEPAPTTPK-EPAPTAPK-KPAPTTPKEPAPTTPK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCP--PAP----PAPPKPKSKAPFPPVPPAPPARELAPPLP--PAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVP-----PAPRALAPLPPAPPAPAEPKSKPPFPPAP-----PAPPCWMLVSAAP 46
                                                                                                                                                                                                                                                                                                                                          FPPFPPAALNPPAP-----PAPPLANSPPLPPAPPTPAGT---PPAAPWPPVPAAPKSKPA
                                                                                                                                                                                                                                                                                                                                                                           EP--APTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAP
                                  LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPA-----PTTPKEPAPTTPKGTAPTTL
                                                                    TTTTPALPAPIPPLPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP--
                                                                                                                                     PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL
                                                                                                                                                                                                       PVPNKIPPAPP---APPVAVAAVLVAPCPPLPPLPNNHPPAPPAAPVPGVPLAPLPNSHP
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                                                                                                                                                                                                                                                                          SPPRPPAP-----PMPATPMEFPPLPPVPPDPISKETPPAPPAPPIPPAPVPIPPVPPLP
                                                                                                  --TTPKEPAPTTPKEPAPTTPKETA----PTTPKGTA----PTTLKEPAPTTP-KKPAPKE
                                                                                                                                                                       ---PKAAAPNTPKEPAP----
   -PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP
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Last annotation updat
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Pred. No. 2.7e-38;
9; Mismatches 361
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Mycobacteriaceae; M
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RESULT
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망
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Best Local
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01-MAR-2001
01-MAR-2001
01-JUN-2001
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Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                Interpro; IPR003882; Pistil_extensin.
Interpro; IPR003965; P.rich_extensn.
PRINTS; PR01217; PRICHEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
SEQUENCE 555 AA; 54219 MW; 6A584P
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                                                                                                                                                                                                                                                                                                                                                   plant hydroxyproline-rich glycoproteins.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF309494; AAG45420:1; -
                                                                                                                                                                                                                                                                                                                                                                                                        Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPAPSMPSAVRVPPSPPIPPAPPAAPRASMPALPPAPPSPPATRLCPPLPPSPPAPNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEPAPTTP---KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET---APTTPKEPAPTTP
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                        PKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKL 433
                                                                             EPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTT 373
                                                                                                         P-APPSPAPPSPAPPSPAPPSPAPPSPAPPSP----
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 PSPPVPPSPSPPVPPSPAPPSPT--
                                                                                                                                                                                                                    189;
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89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TREMBLrel. 17, Last annotation update)
CELL WALL PROTEIN GP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Woessner J.P., Waffenschmidt
                                                                                                                                                                                                                               13.7%; 28.9%;
                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                               Score 707.5; DB 1 Pred. No. 6.2e-38;
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                                                                                                                                                                                                                                                                                       6A584A90465502F5 CRC64;
                                                                                                                                                                                                                     Mismatches 243;
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    -PPSPSPPVPPSPAPPSP--
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В	δÃ	₽	οy	В	Qγ	Дb	δĀ	В	Qy	₽	Ş	₽	Qy
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501 CPGFLTYGTTPIAGYPTGIDATTWPNWKIAGVRINMGAGNKKPKT 545	KTITTTEIMNKPEETAKPKDRATNSKATT-PKPQKPTKAPKKPTSTKKPKT 840	451 GSVANVTIRVAFATEKPALIYSSIELVVYNTGATLIRVPIAANVTRSQIR 500	TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTK 790	394AFDDLNGTSTRPGSASRMVGEPDIAGTKCKGNLKGWMPKPSRNPRWGQAVFSGGRTV 450	PDESTPELSAEPT-PKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETT 732	SPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP	614 TTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKS 673	299 PPTPPTPPSPSPSPPSP-VPPSPAPVPPSPAPPSPAPSPPPSPAPPTPSPSPSP 349	TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTS 61:		PKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT 553	APPVPPSPAPPSPAPPVPPSPAPPSPPSPAPPSPPSPAPPSPVPPSP-A 250	434 APTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT 493

Search completed: April 26, 2002, 16:22:18 Job time: 523 sec

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Perfect score:
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length: 2000000000
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Match
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1: sp_archea:*
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3: sp_fung1:*
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5011
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sp_phage:*
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sp_bacteria:*
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sp_virus:*
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sp_unclassified:*
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1404
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(c) 1993 - 2000 Comp
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Q20007
Q9LIE8
Q41805
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Q9N4S7
Q9I7S1
Q9I6894
076894
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Q9XDH2
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Q9BX49
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       096449 phytophthor
Q9spm0 zea mays (m
020007 caenorhabdi
Q911e8 arabidopsis
Q41805 zea mays (m
p70670 mus musculu
Q9ve19 drosophila
Q9xdh2 mycobacteri
Q9xdh2 mycobacteri
Q9fpq6 chlamydomon
057580 gallus gall
Q9jlli rattus norv
                                                                                                                  092954 homo sapien
09bx49 homo sapien
09bx99 mus musculu
09jm99 mus musculu
09i4s7 caenorhabdi
09i7s1 drosophila
076894 drosophila
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6 rattus norv
caenorhabdi
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573	577	598.5	600.5	605	606.5	607.5	607.5	617	620.5	622	622.5	624.5	624.5	626.5	629	629	632	632	633	641.5	647	647	653.5	654	659.5
11.4	11.5	11.9	•	12.1	12.1	12.1	12.1	12.3	12.4	12.4	12.4	•	•	12.	12.	12.	12.	12.	12.	12.	12.	12.	13		
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## ALIGNMENTS

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Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U70136; AAB09089.1; -.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR002400; GF_cysknot.
Pfam; PF0103; Somatomedin_B.

Pfam; PF0103; Somatomedin_B.

Pfam; PF0103; Somatomedin_B. 2.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Kelleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92954
Q92954;
                                                                                                                                                                                                                                    (In) Preissner K.T., Rosenblatt S., Kost C., Mosher D.F. (eds.);
Biology of vitronectins and their receptors.,
Elsevier Science Publishers B.V. (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEGAKARYOCYTE STIMULATING FACTOR.
PRINTS;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Merberg D.M., Fitz L.J.,
FitzGerald M., Scaltreto
Jacobs K., Turner K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                   Temple P., Giannotti J., Murtha P., J., Kelleher K., Preissner K., Kriz
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM00120; SO; 2.
SMART; SM00201; SO; 2.
SEQUENCE 1404 AA; 151090 MW; AABD77
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                                         KELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVST
                                                                                                         PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT
                                                                                                                                                                                                                                                         DLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK
                     PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPT
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Similarity 100
41; Conservative
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Pred. No. 0;
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RESULT
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O9BX49; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLRel. 17, Last annotation update)
BG174L6.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR).
BG174L6.2.
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submitted (JUL-2000) to the EMBI
EMBL; AL133553; CAC36090.1; -.
SEQUENCE 1404 AA; 151076 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE
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Pred. No. 0;
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EMBL; AB034/30; BAA92310.1; -
MGD; MGI:1891344; Prg4.
InterPro; IPR000585; Hemopexin.
InterPro; IPR000585; P_rich_extensn.
InterPro; IPR001212; Somatomedin_B.
Pfam; PF01033; Somatomedin_B.
Pfam; PF01033; Somatomedin_B.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00127; SOMATOMEDINB.
SMART; SM00120; SOMATOMEDINB.
SMART; SM00120; HX; 2.
SMART; SM00201; SO; 2.
PROSITE; PS000524; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOWEDIN_B; 2.
SEQUENCE 1054 AA; 115991 MW; 4FC648FA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JM99 PRELIMINARY; PRT; 1054 AA.

Q9JM99;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MRNA, COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING
PRECURSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Ikegawa S., Nakamura Y.;
"a novel mouse gene highly homologous to a
"egakaryocyte stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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                                        AKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT
                                                                                      VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVT--TPDTSTTOHNKVSTSPKITTAKP
                                                                                                                                                                                    VKDNKKNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPDPPTTPHSKVATSPKTTAAKP
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                                                                                                                                                                                                                                                                                         Similarity 44.4
23; Conservative
                                                                                                                                                                                                                                                                                                                38.0%;
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                                                                                                                                                                                                                                                                                    Score 1904; Di
Pred. No. 3.5e
33; Mismatches
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4FC64BFA42283235 CRC64;
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.5e-113;
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Y51B11A, I PROTEIN.
                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
      "Genome sequence of the investigating biology.
                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
RCBI_TaxID=6239;
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INTERPO; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DB
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Submitted (MAR-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TTTAPETTSTEPPSSS----TSPVQTTTTTAPETTSTEPPSSSTTPV
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) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 967; DB Pred. No. 8.4e 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmid Y51B11A.";
EMBL/GenBank/DDBJ databases
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                                                                               RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Sabburner M., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Lewis S.E., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlaw R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Dodson K.J., Bousam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Herriandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kranison J.A., Ketchum K.A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Rainert K., Remington K.A., Nixon K., Nixskern D.R., Pacleb J.M.,
RA Merkulov G., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton K.A., Nixon K., Nixon M., Weissenbach J.,
RA Shue B.C., Stapleton M., School S., Zhao Q., Zheng L.,
RA Shue B.C., Stapleton M., School S., Zhao Q., Zheng L.,
RA Shue B.C., Staple T., Zhong W., Zhou X., Smith H.O.,
RA Shu
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CG5228
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Q917S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BERKELEY;
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Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
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                                                           EMBL; AE003495; AAG22353.1;
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         FBgn0030561; CG5228.
1049 AA; 107278 N
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Neoptera; Endopterygota; Diptera;
); Drosophilidae; Drosophila.
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                954DD629E7619671 CRC64;
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                                                                                                                                                                                                                  H.O.,
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TLKPTERTSAQ--PTTLKPTEGTTAKPTTLKPTKGTSGQANNFETKRKERRP ELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEG-ETPHMLLRP

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-GTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGPSAKPTTLKPTERTSAQPT
                            RATNSKATTPKPQKPTKAPK---KPT--STKKPKTMPRVRKPKTTPT---PRKMTSTMP-
                                                          PTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTAKPTTLKPTEGTSAKPTTLKPTE
                                                                               KITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKK--TITTTEIMNKPEETAKPKD
                                                                                                                     PTEGTTAKPTTLKPTEGTSAQPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAK
                                                                                                                                            PEMTTTAKDKTTERDLRTT------PETTTAAPKMTKETATT-----TEKTTES
                                                                                                                                                                              TL--KPTEGT----SAKPTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPTERTSAQPTTLK
                                                                                                                                                                                                                  TIHKSPDESTPELSAEPTP----
                                                                                                                                                                                                                                        TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTRTTAKPT
                                                                                                                                                                                                                                                                  TSDKPAPTTPKE--TAPTTPKEPAPTTPKKPA---PTTPETPPPTTSEVSTPT-TTKEPT
                                                                                                                                                                                                                                                                                                                           APTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK----KPAPKELAPTTTKGPTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLTPT----TPEKLAPTTPEKPAPTTPEELAPT--TPEEPTPTTPEEPAPTTPKAAAPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPA----PTAPKEPAPTTPKETAPTT--PK 423
                                                                                                                                                                                                                                                                                                                                                          KPTTLKPTEGTSAQPTTLKPTEGTSAQSTTLKPTEGTTAKPTTLKPTEGTSAQPTTLKPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKE----PASTTPKEPT---PTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAKET--QSIEKTSAK--DLAPTSKVLAKPT-----PKAETTTKGPALTTPKEPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGTTAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTAKPTTLKPTEG----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                 PTTLK---PTEGTSAKPTTLKPTEGTTAKPTTLKPTDGTTAKPTTLNPTEG
                                                                                                                                                                                                                                                                                                                                                                                       -PKELAPT-----TTKEPTSTTSDKPA------PTTPKGT
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34.6%;
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Pred. No. 7e-52;
5; M1smatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TEGTSAKPTTLKPTEGTSAKPTTLKP
                                                                                                                                                                                                            KALENSPKEPGV--PTTKT---PAATK
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ACCOCC DITION ACCOCCATE AC
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AE003421; AAF45644.1; -. EMBL; AL031028; CAA19845.2; -.
                                                                                                                                                                                                                               "Sequencing the Submitted (JUL-1
                                                                                                                                                                                                                                                             Cadieu E., Dreano S., I
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musciephydroidea; Drosophilidae; Drosophila.
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chromosome of Drosophila melanogaster.";
the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002557; Chitin_binding.
InterPro; IPR002655; P. rich_extensn.
pfam; PF01607; Chitin_bind_2; 2.
pRINTS; PR01217; PRICHEXIN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F
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                      TLKTT----TLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKA-PK
                                                                                                                                               TSIGTTRIPTTTNPQNSTSSTDLTTVTRPPCPDPDSTSDKNTNTACTQELQQVNLLELQS
                                                                                                                                                            RTTPKVTTVIVSTQNPTTTTSKTSTVTI-----TTP-NPSPSTQRPTTTTRQPTSITAST
                                                                                                                                                                                                                    PTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP-TTTKGPTSTTSDK
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                                                 HLLQKLFHIISTTPPSREHAP-
                                                                     KTTER----DLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKIT
                                                                                               PQKQEQFTHTRTHTALTGSRNTLGGQEVPDYMDDAPSSAEAESGQATTAKAPTMSTLAAA
Similarity
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29; Mismatches
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01-MAY-1999 (TrEMBLrel. 10, Last seq)
01-MAY-1999 (TrEMBLrel. 11, Last ann)
01-MAY-1999 (TrEMBLrel. 11, Last ann)
CYST GERMINATION SPECIFIC ACIDIC REP
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Goernhardt B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF061185; AAC72308.1; -.
SEQUENCE 1489 AA; 164037 MW; 764CC79D1C2F5163 CRC64
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Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-JUN-2001 (TrEMBLrel. 17, L
EXTENSIN-LIKE PROTEIN.
                                                                                                                          Stratford S., Barnes W., Golubiewski A., Cotter R., McCormick Hohorst D., Gao M., Showalter A., Bedinger P.A.;
"Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.",
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF159297; AAD55980.1; -
InterPro; IPR001518; LRR.
InterPro; IPR001998; Xylose_isom.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003592; LRR_out.
                                  PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SMART; SM00370; LRR; 3.
           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl Panicoldeae; Andropogoneae; Zea.
NCBI_TaxID=4577;
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                        TPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLS
                                                       PPPMKSPPPPAPISSPPPAP--VKPPSLPPPAPVSSPPPAV
                                                                               QKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ
                                                                                                                                                                                              TKPEMTTTAKDKTTERDLRTTP-----ETTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                                                                                                 XKPLPPP---APVSSPPPVVKSSPPPAPVSLPPPTRKPSPPRTRVSSPRPVVKCCPPPTL 1096
                                                                                                                                                                                                                                                                                                      TPKKPAPKELAPTTTKGPTSTTSDKPAPTT--PKETAPTTPK----EPAPTTPKKPAPTT 647
                                                                                                                                                                                                                                                                                                                                                              KPAPT----TPKGTAPTTP------KEPAPTTPKEPAPTTPK--GTAPTTLKEPAPT
                                                                                                                SPPPPAKSP------PPPA---
                                                                                                                                       STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKP
                                                                                                                                                                                                                                  VSSPPPAPKSLPPPTPVSSP---
                                                                                                                                                                                                                                                       PETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA 707
                                                                                                                                                                                                                                                                                                                                          PPAPVSSPPPTARPLPPPAPVSSPPPVVKSSPPPPTPVSSPPPTPKPLPPPPTPVSSPPPT
                                                                                                                                                                                                                                                                                                                                                                                                   LAPISSPPSEPKSPSSPPMVEKTSPPPATVSSPPPTPKSSPPP---APVSSPPPVVKSSP
                                                                                                                                                                                                                                                                                                                                                                                                                             TTPKETAPTTPKGTA------PTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPPLEPKPSSPPSSVSSPPTTVKSSPPPAPLSSPPMTPKSSSPPAHVSSPPEAEKSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPAPTTPEELAPTTPEEPTTTPEEPAPTTPKAAAPNTDKEPAPTTPKEPAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PAPVS---SPPPLKSSPPPVPESSPPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTPGGPPSSSVPGKPPSVPG------KPAAPAPMPTPHTPPDVSP----EPL-PE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPTLTTSPPPQEKPTPPSTPSKPPPPSPVETLPPPSKSSPPEEPVSSPPQAPKSSSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTTKEPSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASPPPPVKSPPPLAPVSSPSPPVKLPPLPAPGKSTPPPEEEKPTPPTPVKSSPPPEKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEPAPTTTKEPAPTTTKSAPTTPKE----PAP--TTP----KKPAPTTPKEPAPTTPKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPMKSP---PPPARVASPPPLMKSPPPPAPVASPPQPLKSPPPPVLWLSTPSVKSPPPPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTP-KEPAP-----TTTKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIEKTSAKDLAPTSKV------LAKPTPKAETTTKGPALTTPKEPTPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPPATPVKSSPPPAAVVLPPPAKTPSPPAPVASPPPEAPVSSPQPQVKSPPPPAPVASPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPVPAPAPMRMPTLRSPPADEYIPT----PPVPAKSPPGTSPPASRGAPPLQAQPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTP-----KPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
    PKKEEDSTA--
                                                                                                                                                                     ----ELKSSPPPAPVSSPPSAPKSSPPPAPVSLPPPEVKSSPPPAPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- NSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQ
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5; Mismatches 459;
                                                                                                                                                                                                                              ----PPEVKSSPPPTPVSSPPPAPKSSPPPTPVS
-PPAEALPPPSFNDIILPPIMA
                                                                                                             -PMSSLPPPVKSPPPPAPVSSP
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1301
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Query Match

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Best Local
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Q20007;
Q1-NOV-1996 (
Q1-NOV-1998 (
Q1-NOV-1998 (
COSMID F35A5.
F35A5.1.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F
Rarsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F
Rarsons J., Percy C., Rifken L., Woodham R., Sulston J.,
Thomas K., Vaudin M., Vaughan K., Waterston R.,
Waterston A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Ratson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Ratson A. Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Waterston R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
EMBL; U46675; AAB52641.1;
SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mb of contiguous nucleotide sequence from chromosome ans.
                                                                                                                                                                                                                                                                                                 KNRTKK-KP----TP----KPPVVDEAGSGLDNGD----FKVTTPDTSTTQHNKVSTS
                                                                                                                                                                                                                                                                     KNPTKKWKPPWEDETPVEEVKEPPVPEKKAPVLKKKDPAPAAKARDPSPSKAAPKKVEPS
                            TPVKNPVKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKP
                                                                                       EAPAKKTPVLKRKEPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPA-
                                                                                                                   KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP
                                                                                                                                                 PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP
                                                                                                                                                                              ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA--
                                                                                                                                                                                                            SPYVPPTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPS
                                                                                                                                                                                                                                       PKITTAKPI-NPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK
                                                            TTTKEPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JAN-1996)
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                                                                                                                                                                                                                                                                                                                                  Conservative
 APTTPKKPAPTTPKE----PAPTTPKEPTPTTPKEPAPTTKEPAPTTPK-EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                 16.0%;
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                                                                                                                                                                                                                                                                                                                                  102;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                               Score 802; DB 5;
Pred. No. 2.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                             PTTPKEPAPTTTKEPAPT----
                                                                                                                                                                                                                                                                                                                                  Mismatches 414;
                                                                                                                                                                                                                                                                                                                                                                                                           07F6B0D292C1799F
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RESULT
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ID Q9LIE8
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QSLIES
                                                                                 SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
Kaneko T., Kato T., S.
Submitted (MAR-2000)
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  SEQUENCE FROM N.A. STRAIN-COLUMBIA;
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DNA Res. 7:217-221(2000).
EMBL; APO01306; BAB03062.1; -.
INTERPRO; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1480 AA; 147153 MW; DIACOC79F155E732 CRC64;
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Nakamura Y.;
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ODTTPFKITTLKTTTLAPKVTTTKKT----ITTTEIMNKPEETAKPKDRATNSKATTPKP
                                                                                     TPPIAKPPVATPPTTAPPTATPPVAKPPVATPPIATPPTAKPPILTPPISKPPVATPPAA
                                                                                                                                                                                                            KPPVAT---PPTATPPIATPPIATPPVVTPPTATPPVATPPIAKPPTTI--PPTATPPVA
                                                                                                                                                                                                                                                                                                        TPKEPAPTTPKEPAPTTPKETAP--TTPKGTAPTT---LKEPAPTTPKKPAPKELAPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTKSAPTTTKEPAPTTTKSAPTTPKEP--SPTTTKEPAPTTPKEPAP---TTPKKPAPT
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                            TPPITTPPPAKPPVATPPIATPP---IAKPPVATPPIATPPIATSPVAKPPVAIPPIKTPP
                                                         TKPEMT-TTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT
                                                                                                                                                  MPPIATPPTAKPPIATPPIAIPPVAKPPVVTPPTATPPIATPPIAKSPVATPPTATPPVA
                                                                                                                                                                       APKELAPTTTKGPTST--TSDKPAPTTPKETAPT-TPKEPAPTTPKKPAPTTP-----E
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Pred. No. 3.9e-43;
4; Mismatches 505;
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STRAIN-B73; TISSUE-POLLEN;
Rubinstein A.L., Broadwater A.H.,
Submitted (JUN-1994) to the EMBL//
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SEQUENCE
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InterPro; IPR003592; LRR_o
Pfam; PF00560; LRR; 3.
SMART; SM00370; LRR; 4.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl.
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
EXTENSIN-LIKE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4577;
             719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN
        SP--PKEPVSSPPQTP----KSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSP----
                                                      APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTPKEPAPTTTKSAPTTPK
                                                                                                                                                              PKKPAPTTPKEPAPTT-----PKE---PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV
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                                                                                                             PAKSTPPPEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPPQEKPTPPSTPSKP-PSSPEKP
                                                                                                                                                                                                               PPAPVASPPPPVKSPPPPTPVASPPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPP
                                                                                                                                                                                                                                                                 PTTTKSAPTTP--KEPAPTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP-KEPAPTT
                                                                                                                                                                                                                                                                                                                     SPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPPVKSP--PPPTLVASPPPPVKSPP
                                                                                                                                                                                                                                                                                                                                                                         ----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPA
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120980 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ
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MW; 2C77C7F8D7130149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.H., Lowrey K., Bedinger P EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 784;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               -SPPPPVKTTSPPAPIG----SPSPPPPVSVV
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8.6e-42;
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InterPro; IPR002715; NAC.
InterPro; IPR003037; TS-N.
InterPro; IPR003037; TS-N.
Pfam; PF01849; NAC; 1.
Pfam; PF02094; TS-N; 1.
SEQUENCE 2187 AA; 220599
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220).
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P70670;
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MEDLINE=96312450; PubMed=8698236;
Yotov W.V., St-Arnaud R.;
Potferential splicing-in of a proline-rich exon into a muscle-specific transcription factor.";
Genes Dev. 10:1763-1772(1996).
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.CB. (Mouse).
.us musculus (Mouse).
...taryota; Metazoa; Chordata; C:
...taryota; Metazoa; Rodentia; S
                                                                                                                                                                                                                   34 VTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKE-----TSLTVNKETT
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                                                    APSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPS----PQKTPKSVSLKGAPA
                                                                                                         VETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA
                                                                                                                                                                 VQSPKVDPIMSDVTPTSPKKTSATAV-PK-----DTSATLSLKSVPAVTSLSPPKAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPPPAP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U48364; AAB18734.1; -. U48363; AAB18732.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·--VKPPSLP-PPAPVSSPPPVVTPAPPKKEEQSLPPPAES
                                                                                                                                                                                                                                                                                                                                                                                                              1.
220599
                                                                                                                                                                                                                                                                                                    15.5%;
27.7%;
        PKE---
                                                                                                                                                                                                                                                                           122;
                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                    Score 776; DB 11;
Pred. No. 1.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              003646AA864DEBFD
     -PTPTTPKEPASTT - - - - -
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; Murinae; Mus
        ·--PKEPTPTT
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GE DI DI AC

Q9VEL9

PRELIMINARY;

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CG4090

O9VEL9; 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CG4090 PROTEIN.

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                                                               DSHISPVS-DACSTGTTTP
                                                                                                                                                                                                                                                                        TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKEPAPTTPKEPAPTTPKKPAPTT--PKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKR
                                                                                              LVEVNPKSEDAGGAEGETP
                                                                                                                                                     APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK
                                                                                                                                                                                         QTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP----
                                                                                                                                                                                                                                                     T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP
                                                                                                                                                                                                                                                                                                                 KNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSIK-PVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPTPTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP----SPQKIPKVAGPKEASATPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPASKGVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGEISPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGVTAVPPETSLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLETPSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APTT -- TKSAPT ----
                                                                                                                                                                                                                    DTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTK
                                                                                                                                                                                                                                                                                                                                              TSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA
                                                                                                                                                                                                                                                                                                                                                                             PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV
                                                                                                                                                                                                                                                                                                                                                                                                          PKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP-----PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                             VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTTPKGTAPTTLKEPAPTTP--
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                                                                                                                             -PKKASSSKRASTLP-
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                                                                                                                              ATTLPSLKEASVLS-
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RA Adams H.D., Celliker S. E., Lil P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Peiffer B.D.,
RA Ballew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Butler H., Cadleu E., Center A., Chandra I.,
RA Groy B., Delcher A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gerstell J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dutbin K.J., Evangelista C.C., Perraz C., Ferriara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Nixon K., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Nixon K., Nusskern D.R., Durin Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parleb J.M.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Mang Z.-V., Wassarman D.A., Weinstook G.M., Weissenbah J.,
RA Spier E., Spradling A.C., Stoplet F. E., Shen H..,
Ra Shoe B.C., Siden K.Banss I., Simpson M., Strong R., Sun E.,
RA Hostin D., Strong W., Strong R., Sun E.,
RA Short S., Sheller F., Zh
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 281; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoua, Linched, Brachycera; Muscomorpha; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                  1071
                                                                                                                                                                                                                                                              1023
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                                                                                                                                                                                                                                                                                                                           NKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRP
NNNNQGSSSSSSSSSSSSKPNPSETCKVNGQFIGDRSDCAKFYRCVDNDRGGFNMVPF
                                                                 ----EKTSAKDLAPTSKVLAKPTPKAETTTKGP-----
                                                                                                                                  SSSSNSGSSSNTGSSSNSGASSSGGSSNQGSSSNSGSSSGSNSSGNQSTSSSTSSSSSSS
                                                                                                                                                                                            SLPPNSDTSKETSLTVNKETTV - - - ETKETTTTNKQTS - - - - TDGKEKTTSAKETQSI - -
                                                                                                                                                                                                                                                              NHPDQIQTKPLKCKKVVSQGGSSSN-----STSNSSSSSNNSGSSSNSGSSSS-----
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A; 219547 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 739; DB 5;
Pred. No. 4.2e-39;
98; Mismatches 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B91018E5551A5D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2112;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                             316;
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                                                                 143
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Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;

Corynebacterineae;

Mycobacteriaceae;

Mycobacterium

Actinobacteridae;

Actinomycetales; NCBI\_TaxID=1773;

01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, PROLINE-RICH MUCIN HOMOLOG.

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Q9XDH2; Q9XDH2

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RESULT
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ID Q9XDH2
AC Q9
AC Q9
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EMBL; AF071081; AAD41594.1; -
InterPro; IPR002951; Atrophin.
InterPro; IPR002951; Atrophin.
InterPro; IPR002955; P.rich_extensn.
InterPro; IPR003882; PIstil_extensin.
PRINTS; PR01222; ATROPHIN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSN.
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STRAIN-H37RV;
Espitia C., Laclette J.L.,
Espitia C., Singh
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                          TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN
                                                             --PAPPAPPAPPSALPFVNPPA
                                                                           KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI
                                                                                                                                                                                                                                                                                                      TTTTPALPAPIPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP--
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   PAAPPAPPAPPVRATTP-
                                                                                                                      --PAPPAPPTPPKLLS--ANPPCPPVPPAPNRPPAPPAPPAPPELPAPPDPPTPPVANSP
                                                                                                                                                   KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSAEPTPKA---LENSP
                                                                                                                                                                                                                KEPAPTTP----KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET---APTTPKEPAPTTP
                                                                                                                                                                                                                                               --PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP
                                                                                                                                                                                                                                                                         LAPTITKEPTSTTSDKPAPTTPKGTAPTTPKEPA-----PTTPKEPAPTTPKGTAPTTL
                                                                                                                                                                                                                                                                                                                                    --TTPKEPAPTTPKEPAPTTPKETA----PTTPKGTA----PTTLKEPAPTTP-KKPAPKE
                                                                                                                                                                                                                                                                                                                                                                  PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL
                                                                                                                                                                                                                                                                                                                                                                                                  ---PKAAAPNTPKEPAP---
                                                                                                                                                                                                                                                                                                                                                                                                                              PVPNKIPPAPP----APPVAVAAVLVAPCPPLPPLPNNHPPAPPAAPVPGVPLAPLPNSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPPRPPAP----PMPATPMEFPPLPPVPPDPISKETPPAPPAPPIPPAPVPIPPVPPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75034 MW;
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Pred. No. 5.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39168EC45A5916F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             new member of the PGRS family in Mycobacterium tuberculosis.
                                                             --PPTPAAPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PAPPCWMLVSAAP
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PPAPPAPPAPN
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Best Local S
Matches 189
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ de EMBL; AF309494; AAG45420.1;
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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NCBI_TaxID=3055;
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01-MAR-2001 (TrEMBLrel. 11, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
VEGETATIVE CELL WALL PROTEIN GP1.
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Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii.
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                                                TTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKS
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                                                                                                   PPTPPTPPSPSPPSP---PAPSPAPVPPSPAPPS----PAPSPPPSPAP---
                                                                                                                                                    TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTS
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                                                                                                                                                                                                                                                                                                              -APPVPPSPAPPSPPSPAPPSPPSPAPPSPPAPPSPVPPSP-A
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28.98;
-PSPSPSPSPSPIPSPSPKPSPSPVAVKLVWADDAI----
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Pred. No. 1.3e-37;
6; Mismatches 243;
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C FC INANAMOREMETA CONTINUE TELEVISION OF THE CO	501 CPGFLTYGTTPIAGYP	791KTITTTEIMNKPEETAKPKDRATNSKATT-PKPQKPTKAPKKPTSTKKPKT 840	451 GSVANVTIRVĀPATEKPALIYSSIELVVYNTGATLIRVPIAANVTRSQIR 500	733 TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTK 790	394AFDDLNGTSTRPGSASRMVGEPDIAGTKCKGNLKGWMPKPSRNPRWGQAVFSGGRTV 450	674 PDESTPELSAEPT-PKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETT 732
			00	90	50	32

Search completed: April 26, 2002, 16:21:42 Job time: 487 sec

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Perfect score:
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Gapop 10.0 ,
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                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Relleher K., Giannotti J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U70136, AAB09089.1; -.

InterPro; IPR000585; Hemopexin.

InterPro; IPR000585; Hemopexin.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.

InterPro; IPR001212; Somatomedin_B.
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Merberg D.M., Fitz L.J., Temple P., Giannotti J., Murtha P., FitzGerald M., Scaltreto J., Kelleher K., Preissner K., Kriz Jacobs K., Turner K.;

(In) Preissner K.T., Rosenblatt S., Kost C., Wegerhoff J., Wosher D.F. (eds.);

Biology of vitronectins and their receptors., pp.45-52, Elsevier Science Publishers B.V. (1993).
                     Pfam; PF00045; hemopexin; 2. Pfam; PF01033; Somatomedin_B; 2.
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Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C., Turner K.J., Fitz L.J., Calvetti J., FitzGerald M., Kriz M.J., Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T., Bhatia S., Kriz R., Hewick R., Clark S.C.;

Blood 78:279-279(1991).
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PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
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03	980 PQKPTKAPKKPTSTKKPKTMPRVPKKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN	Qy	
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Db 236 PTTPHSKVATSPKTTAAKPVTPKPSLAPNSETSKEASLASNKETTVETKETTATNKQSSA 295  Qy 258 DGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEP 317	TNKOTST 2	SSSSTIR 1	AP 1	QY 26ELSCKGRCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAP 79	Db 1 MGWKILPVCLSLLLPVVLIQQVSSQDLSSCAGRCGEGYSRDATCNCDYNCQHYMECCPDF 60	2	Query Match 51.1%; Score 3716.5; DB 11; Length 1054; Best Local Similarity 54.5%; Pred. No. 2.2e-233; Matches 772; Conservative 58; Mismatches 171; Indels 415; Gaps 26	PROSITE; PS00024;	DR PRINTS; PRO1217; PRICHEXTENSN. DR PRINTS; PRO0022; SOMATOMEDINB.	InterPro; IPR001212; Somatomedin_B	EMBL; AB034730; BAA92310.1; MGD; MGI:1891344; Prg4.	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases	Ikegawa S., Nakamura Y.;	RP SEQUENCE FROM N.A.	Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Mur NCBI_TaxID=10090;	Eukaryota; Metazoa; Chordata; Craniata; Ver	PRG4.	MRNA, COMPLETE CDS, SIMI	01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,	01-OCT-2000 (TrEMBLrel. 15,	RESULT 3 Q9JM99	Db 1381 PSRTARAITTRSGQTLSKVWYNCP 1404	Qy 1340 PSRTARAITTRSGQTLSKVWYNCP 1363	Db 1321 SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1380	Qy 1280 SPARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKDQYYNIDV 1339	Db 1261 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGETTQVRRRRFERAIGPSQTHTIRIQY 1320
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                                                                                                                                                             KPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTP
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                                                                         GIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDVVDPGYPKQIVKGFGGLTGKIVAALSI
                                                                                                    EAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVP
                                                                                                                                                                                                    QVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKAT-
                                                                                                                                                                                                                                     PTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTT
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                                                                                                                                                                                                                                                                                -----KEPEPTTPKEPEP-----TTRKEPEPTTPKEPEPTTPKEPEPTT
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              AKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIG
                                                                                GIPSDIDTVETRCNCEGKTEFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALST 1208
 AFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP
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                                                                                                                                                                                            -----TTLKATTLAPKVTAPAE-----EIQNKPEETTPASEDSDDSKTTL
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Best Local Similarity
Matches 320; Conserv
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
SUPERFICIAL ZONE PROTEIN (FRAGMENT).
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EMBL; AF056218; AAD13404.1; -
InterPro; IPR000585; Hemopexin.
Pfam; PF00045; hemopexin; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
SMART; SM00120; HX; 2.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=ARTICULAR CARTILISCHER B.L., Hughes Aydelotte M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                        σ
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                                                                                                                                                                                                                                                                       S-LPEAMLQTTTRPTPTPNSEIIDVNSENEDGDAAEGEKPHMIFRPPVLTPIVIPGTEII 122
                                                                                                                                                                                                                                                                                                                                  SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYL 1084
                                                                                                                                                                                                                                                                                                                                                                 RAIGPSOTHTIRIQYSDARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGY
                                                                                                                                                                                 ALSTAKYKNWPESVYFFKRGGSIQQYIYKOEPVQKCPGRRPALNYPVYGEMTQVRRRREE 1264
                                                                                           DYYALSKDQYYNIDVPSRTARAITTRSGQTLSNTWYNCP
                                                                                                     DYYAFSKDQYYNIDVPSRTARAITTRSGQTLSKVWYNCP 1363
                                                                                                                                     RAIGPSQVHTIRIHYTPVRVPYQDKGFLHNEVKVSTLWRGLPNVVTSAISLPNIRKPDGY
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Hughes C.E., Kuettner K.E.,
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Last annotation update)
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Pred. No. 9.3e
24; Mismatches
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Q9N4S7; Q9N4S7; 01-OCT-2000; 01-OCT-2000;

(TrEMBLrel. (TrEMBLrel. PRELIMINARY;

15, 15,

Last Created)

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Best Local S
Matches 332
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Waterston R.;
Submitted (MAR-2000) to the EMBL/GenBank/Luc.
EMBL; AC006797; AAF60743.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
1079.AA; 110532 MW; 8DBDE3824CF80CAl CRC64;
662 ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTT
                              468
                                                   604
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                              154 QKKLKVKDNKKNRTKKKPTPKPPVYDEAGSGLDNGDFKV-----TTPDTSTTQ-HNKV
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Y51B11A.1 PROTEIN.
Y51B11A.1.
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                     TTTAPETTSTEP-PSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPE-TTSTES
                                                                 SSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTSTEP----PSSSTTPVQTT
                                                                                PEELAPTTPEEPTTTPEEPAPTTPKAAAPNTPKEP--APTTPKEPAPTTPKEPAPTTPK
                                                                                                             APETTRTEPPSSSTTPVQNTTTTAPETTSTEPPSSSTTPVQTTTTT----APETTSTEPP
                                                                                                                            APTTTK--EPAPTTTKSAPTTPKEPSPTTTKEP-APTTPKEPAPTTPKKPAPTTPKEPAP
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                                                                                                                                                                            PTAPKKPAPTTPKEPAPTTPKEP------APTTTKEPSPTTPKEPAPTTTKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 177;
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	01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CG5228 PROTEIN.	01-MAR 01-MAR 01-JUN 01-JUN CG5228 CG5228	S E E E E E
	6 S1 PRELIMINARY; PRT; 1049 AA.	RESULT 6 Q917S1 ID Q917S1 AC 0917S1:	RES Q91
	PARRITEVWGIPSPIDTVETRCNCEGKTFFFKDSQYWRFTN 1180  YNVPTGLE-IWPEINCEGNKWSYNN 1064	1140 1041	D
1139 1040	AFSFVSTFDIGTCTAILTCIYTSEGGISNL-NATLFIGLSDGSSIDLPF	993	) B 4
1103 992	GAEG - ETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETN	933	B 5
1057 932	TMPRVRKKTTPTPRKMISTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAG	998 879	4g .
997 878	TLAPKVTTTKKTITTTEIMNKPEETA-KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPK :   :   :   :   :   :   :   :   :   :	939 821	9 dg v
938 820		883 763	Db Qy
882 762	5 PTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERD	825 703	Db
824 702	8 APTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKE :	643	Db 04
777 642	1 PKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKP-	721 586	Db Qy
585		526	ф

OCCOOCA OCCOOC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Ffeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C.G., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferriez C., Ferriera S., Fleischmann W., STRAIN-BERKELEY; SEQUENCE FROM N.A. Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.C., Mobarry C., Morris J., Moshrefi A.,
RA McIntosh T.C., Mishina N.V., Mobarry C., Muzny D.M., Nelson D.L.,
RA Rainert K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong G., Zhao Q., Zheng L.,
RT "The genome sequence of Drosophila melanogaster.";
RT "The genome sequence of Drosophila melanogaster.";
SEQUENCE 1049 AA; 107278 MW: 954DD629E7619671 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTAKPTT-----LKPTEGTSA-----KPTTLKPTE--GTTAKPTTLKPT---EGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIGTTAKPTTLKPTEGTSAKPTTLKPTEGTSAKPTTLKPT-----EGTTAKPTTLKPTE
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                                                                          TPKETAPTT - - PKKLTPTTPEKLAPTT - - PEKPAPTTPEELAPT - - TPEEPTPTTPEEPA
                                                                                                                                                                                                                                TTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPA---PTTTKSAPTTPKEPSPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKPTEGTSAKPTTLKPTEG----TSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPT
                                                                                                                 AKPTTLKPTEGTTAKPTTLKPTKGTKGTSAKPTTLK-PTEGTTAKPTTLKPTEGTTAKPT
                                                                                                                                                      KEPAPTTPKE----PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKE----PAPT
                                                                                                                                                                                               TTAK----PTTLKPTEGTTAK----PTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTT
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PTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTP
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkoya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            076894;
01:NOV-1998 (TrEMBLrel: 0
01:NOV-1999 (TREMBLrel: 1
01:JUN-2001 (TREMBLREL: 1
EG:56G7.1 PROTEIN:
EG:56G7.1 OR CG14796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
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(TrEMBLrel. 12, Last sequence up)
(TrEMBLrel. 17, Last annotation)
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Matches 319
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Science 287:2185-2195(2000).
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                                                         337
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Caddeu E., Dreano S., Lelaure V., Mottier S., Galibert F.;
"Sequencing the distal X chromosome of Drosophila melanogaster.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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THNTSPDTKTTIRSTTLSPKTTTTPSTTTPSTTTPST----TTPSTTTPST----
                                                                                                                                             TTTAVTKSTPKISSTEQHSTTTAKTTTTKRPTTVTEKTSSATEKPRTTVVTTTTQKRSTT
                                                                                                                                                                                                                                                                               DT-----SKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTS
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26.5%; Pred. No. 9.8e-50;
Live 154; Mismatches 520;
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                                                                                                                                                                          SIQQLASTQKRSIPPKTLVTHNTTKEPED-SEYYDSETSEQYTDEDNEVLDKTQPRAMSS
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                                                                                                       ELSAEPTPKA-LENSPKEPG-----VPTTKTPAATKPEMTTTAKDKTTERDLRTTP----
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     ETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTT-
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AA; 164037
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Pred. No. 5.7e-48;
5; Mismatches 509
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REDLINE-94150718; PubMed-7906398;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Ainscough R., Anderson K., Evello A., Fulton L.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

A Parsons J., Percy C., Rifken L., Roopra A., Sulston J.,

RA Phierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"1.2 M of contiguous nucleotide sequence from chromosome III of C.

"T elegans."
                                                                                                      Query Match
Best Local S
Matches 313
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01-NOV-1998
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Meladerinae; Caenorhabditis.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                             Waterston R.;
Waterston R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
EMBL; U46675; AAB52641.1; -
SEQUENCE 1274 AA; 138065 MW; 07F6B0D292C17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                         Local Similarity es 313; Conserv
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PSPKKAAPSKEHDPIVPPTPIKNPAKKWKPPWEDDEVPTEEIKEPEPATRKVPALKKKEP
                                                   PSSKKAPPPSGASQTIKSTTKRSP----KPP---NKKKTKKVIESEEITEEHSVSENQES
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Last annotation update)
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                                                                                                            Score 846; DB 5;
Pred. No. 6.7e-47;
9; Mismatches 455;
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                               977 TPKPQKPTKAPKKPTSTKKPKTMPRVRKPK------TTPTPRKMTSTMP 1019
                                                                                                                                                             865 AT-----KPEMTTTAKDKTTERDLRTTPETT--TAAPKMTKETATTTEKTTESKITATT 916
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                                                                                                                                                                                                                                                                                                                                                           735 TTPKGTAPTTLKEPAPT-----TPKKPAP-----KELAPTTTKGPTS-----TTSDK 776
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

Panicoideae; Andropogoneae; Zea.

NCBL_TaxID=4577;
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 TISSUE-POLLEN;
Stratford S., Barnes W., Golubiewski A., Cotter R., McCormick Stratford S., Barnes W., Showalter A., Bedinger P.A.;
Hohorst D., Gao M., Showalter A., Bedinger P.A.;
"Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF159297; AAD55980.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR001998; Xylose_isom.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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RCFESFERGRECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPB CQCAPVLARPVEDCSKHVCAGYPTPPBP QCAPVLARPVEDCS	Query Ma Best Loc Matches	DR Pfam; PFOLDR PRINTS; PFOLDR PRINTS; PFOLDR PROSITE; I DR SMART; SMART; SMC SQ SEQUENCE	Inter
EVHNPTSPPSSK-KAPPPSGASQTIKS 90	11.2%; Score 816; DB 10; Length 1315; imilarity 23.5%; Pred. No. 6.1e-45; ; Conservative 106; Mismatches 486; Indels 270; Gap	1PR003594; 0560; LRR; () 001217; PRI0 PS00172; XYI 00370; LRR; 1315 AA;	Pro; IPR002965; P_rich_extensn.

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Best Local Sim
Matches 311;
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MEDLINE-96312450; PubMed-8698236;
YOCTOW N.V., St-Arnaud R.;
"Differential splicing-in of a proline-rich exon into a muscle-specific transcription factor.";
Genes Dev. 10:1763-1772(1996).
EMBL; U48364; AAB18732.1; -.
EMBL; U48363; AAB18732.1; -.
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InterPro: IPR003037; TS-N.
Pfam; PF01849; NAC; 1.
Pfam; PF02094; TS-N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
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P70670;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE (ALPHA-NAC, MUSCLE-SPECIFIC FORM GP220).
             354
                                                             941
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----EPAPTTTKEPAPTTPKEPAPTTTKEPAPTT--TKSAPT--
                                          QHV----PPTSPPKSPVSDTLSGALTSPPPKGPPATLAETPTYPKKSPKPAASKKTPATPS
                                                                                                                                                                            T-----TVETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKETPKA
                                                                             ETTTKGPALITPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKE-PAPTTTKSAPTTPK 353
                                                                                                                                            TLATSIPKVTSPSPQKTPKSVSLKGAPAMTSKKAT---EIAASKDVSPSQ--FPKEVPLL
                                                                                                                                                                                                                                               -----DTSATLSLKSVPAVTSLSPPKAPVAPSNEATIVPTEIPTSLKNALAAATPKE
                                                                                                                                                                                                                                                                                                                                              KTPEVTASRLISAVQSPKVDPIMSD-----VTPTSPKKTSATAVPK--------
                                                                                                                                                                                                                                                                                            GDFKVTTPDTSTTQHNK----VSTSPKITTAKPINPRPSLPPNSDTSKETSL--TVNKE
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27.48;
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220599 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 812; DB 11;
Pred. No. 1.9e-44;
8; Mismatches 449;
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Sciurognathi; Muridae;
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; Murinae; Mus
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Q9VEL9;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
CG4090 PROTE
CG4090.
                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           1731
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                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                          Brachycera; Muscomorpha;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., I. P.W., Hoskins R.A., Galle R.F., RA Adams M.D., Charles M. Henderson S.N., Gecry R.A., Levis S.E., R.C., Radards S., Ashburner M., Henderson S.N., RA Ballew R.A., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D., RA Wan K. H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.A., Burtis K.C., Bassa A., Baxendale J., Bayraktargiu L., Beasley E.M., RA Ballew R.M., Benss P.V., Berman B.P., Bhandari D., Boshakov S., RA Beeson K.Y., Benss P.V., Berman B.P., Bhandari D., Davles P., Distakov S., RA Ghory J.M., Cawley S., Dahlke C., Davenport L.B., Davles P., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., RA Borkova D., Betcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gund R.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gund P., Harris M., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C., RA Liu X., Mattel B., McIntosh T.C., McIeod M.P., McPerson D. A., Ketchum K.A., Linkov P., Lei Y., Levituky A.A., Li J., Li Z., Llang Y., Lin X., RA Lasko P., Lei Y., Levituky A.A., Li J., Li Z., Llang Y., Lin X., RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Wilshina N.V., Mobarry C., McIeod M.P., McPerson D.L., Ra Ra Lasko P., Lei Y., Levituky A.A., Li J., Li Z., Llang Y., Lin X., RA Ra Harlis S.M., Moy M., Murphy B., Murphy L., Muzry D.M., Nelson D.L., Ra Ra Lasko P., Selon K., Sungers R., Wolston K., Sungers M., Skupski M.P., Smith T., RA Ra Ra Lasko P., Selon R., Selon R., Skupski M.P., Smith T., Ra Ra Ra Lasko P., Selon R., Selon R., Skups
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Best Local
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Interpro; IPR002557; Chitin_binding.
Interpro; IPR002557; Chitin_binding.
Pfam; PF01607; Chittin_bind_2; 10.
SMART; SM00494; ChitBD2; 11.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                  1065
                                                                                                                                                                                                                                                   1012
                                                                                                                                                                                                                                                                                                                                953 OSSSSNOTSSSTTOKPFKPAEKCESEETFLADNENCSKFYRCVDNGKGGFTKV-SFTCPP 1011
                                       250 TINKQTSTDGKEKTTSAKETQSIEKTSAK-DLAPTSKVLAKPTPKAETTTK----
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 313; Conserv
                                                                                                                                                                                                                                                                                                                                                                         21 QVSSQELSCKGRCFESFERGRECDCD-----AQCKKYDKCCPDYESFCAEVHNPTSPP 73
                                                                                                                                                                                                                                                                                          74
TSSSSSSNNNNNQGSSSSSSSSSSSSSTSSKPNPSETCKVNGQFIGDRSDCAKFYRCVDNDR 1182
                                                                                                                      FKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETT 249
                                                                                                                                                                                                       SSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGD 189
                                                                                                                                                                                                                                                 NTLWDPEANSCNHPDQIQTK-----PLKCKKVVSQGGSSSNSTSNSSSSSNNSGSSSN 1064
                                                                                                                                                                                                                                                                                      SSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVI----ESEETTEEHSVSENQESSSSS 129
                                                                                     SSNSGASSSGGSSNQGSSS
                                                                                                                                                                  SGSSSS-----SSSNS-----
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219547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 786.5; DB 5
Pred. No. 8.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                            NSGSSSGSNSSGNQSTS----SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                              380;
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                                                                                            1122
                                                      299
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Q41 AC DT DT AC OC		рь Оу рь	Qy Db	Db Oy	Qy Qy	Qy Db Qy	Qу	Qy Db	QУ	Qy db	ОУ	ОУ
80	979 KPOKPTKAPKKPTSTKKPKTMP 1000	SSPETTTTVASETITITSGISPETTTT 1901	99 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKAL 16 NCSSGQTTTPGTTTEPGTTESTTSSGKPETTSKAP 59 TTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTT 1	TTTT-LPSTTDAIQEPTTSKKPEPTTTESPESSTPEG -PAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT -      : : :       : :       : :	PKEPAPTT-PKEDAPTTPKETAPTTPKGTAPTT     :	527 PAPTIPKKPAPITPKEPAPITPKE-PAPITTKKPAPTAPKEPAPITPKETAPT 578	1.6 TKEPAP	459 PTTPKEPAPTTT	399 PKKPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTAPKKPAPTTPKEPA 458	376TKEPAPTTTKSAPTTPKEPAPTT 398 1298 NNCSKFYRCVRNNKGGFTSIPFQCGAGTVWDQDLQTCNHNFNNCSTGTESTTPKPPCE 1355	329 TIKSAPTIPKEPAPTITKSAPTIPKEPAPTIPKEPAPTIPKEPAPTT	300GP

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Best Local
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                                 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases. EMBL; 234465; CA884230.1; -. Mendel; 14346; Zeama; 2368;14346. InterPro; IPR001611; LRR. InterPro; IPR001612; LRR. Out. Pfam; PF00560; LRR; 3.
                                                                                                                                                                      944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399
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                       SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKOKTTERDLRTTPET
                                                 KSPPPPAPISSPPPPVKSPPPPAPVS--SPPPPVKSPPPPAPVSSPPPPIKSPPPPAPVS
                                                                                                        MSSPPPPEVKSPPPPAPVSSPPPPPVKSPPPPPPPPPV---PPVKSPPPPAPVSSPPPPV
                                                                                                                                                              VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA---PKSSPPPAP
                                                                                                                                                                                                                                                                        LAPKSSPPHYVVSSPPPVVKSSPPPAPVSSSPPLTPKPASPPAHVSSPPEVVKPSTP--PA
                                                                                                                                                                                                                                                                                                  TTPKETAP----TTP----KKLTPTTPEKLAPTTPEKPAP----TTPEELAPTTPEEPT
                                                                            -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL
                                                                                                                                 -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
                                                                                                                                                                                  LKE---PA-----PATTPKK----PAPKELAPTTTKE----PTSTTSDKPAPTTPKGTAPTTP
                                                                                                                                                                                                                    PTTVISP-PSEPKSSPPPTPVSLPPPTVKSSPPPAMVSSP-PMTPKSSPPPVVVSSPPPT
                                                                                                                                                                                                                                              PTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT
                                                                                                                                                                                                                                                                                                                              PPAPLSSPPPAPQVKSSPPPVQVSSP-PPAPKSSPPLAPVSSPPQVEKTSPPPAPLSSPP
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--VKPPSLP-PPAPVSSPPPVVTPAPPKKEEQSLPPPAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 POTENTIAL.
120980 MW; 2C77C7F8D7130149 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SPPPPVKTTSPPAPIG----SPSPPPPVSVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 784; DB 10;
Pred. No. 6.6e-43;
9; Mismatches 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1188;
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                        889
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                                                                                                        1057
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OS MYCODA
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RN [1]
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RR SEQUEN
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RA Zhang
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RA Zhang
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DR Interp
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Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Espitia C., Laclette J.L., Mondragon-Palomino M., Martens A., Zhang Y., Moreno C., Singh M., "Cloning and characterization of a new member of the PGRS family is a useful marker of polymorphism in Mycobacterium tuberculosis. Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; APO71081; AAD41594.1; InterPro; IPR002951; Atrophin.
InterPro; IPR002952; P.rich_extensn.
InterPro; IPR003882; Plstil_extensin.
746 KEPAPTTP---KKPAPKELAPTTTKGP-TSTTSDKPAPTTPKET---APTTPKEPAPTTP
                                                                                                    432
                                                                                                                                                           692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01222; ATROPHIN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
SEQUENCE 763 AA; 75034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XDH2;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                   374
                                                                                                                                                                                                                                                                        642
                                                                                                                                                                                                                                                                                                         314 PAPPSAPVPGVPLAPLPISGRPVSVWKGSFTTLSTFCCRVCSGEVLAGALNPSRPSRSPL
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NCBI_TaxID=1773;
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                                                                                  --PIPPGKPWTTPPLAPAPPEPK-TVPVLPPGPSCPPSEKPNPPAPPEPPEPKSSPALPP
                                                                                                                                                                                               TTTTPALPAPIPPLPPLPPLPINTAVPPIPPLPPVTALAPPLPPLAPLPISPGVPPAP--
                                                                                                                                          LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPA-----
                                                                                                                                                                                                                                           --TTPKEPAPTTPKEPAPTTPKETA----PTTPKGTA----PTTLKEPAPTTP-KKPAPKE
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Qу	Оу	ОУ	Оу	Db Qy Db
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1024 TSRIAEAMIOTTTRPNQTPNSKLVEVNPKSEDAGGAEGET 1063 	973 SKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNP 1023	913 TATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATN 972	KEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI 912	489 APPAPSMPSAVRVPPSPPIPPAPPAAPRASMPALPPAPPSPPATRLCPPLPPSPPAPNSP 548 799 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSP 852 111
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Search completed: April 26, 2002, 16:29:14 Job time: 569 sec

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Listing first 45 summaries
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                   Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
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10: sp_plant:*
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Q77765 bos taurus
Q97487 caenorhabdi
Q91781 drosophila
Q94781 drosophila
Q96449 phytophthor
Q99007 caenorhabdi
Q911e8 arabidopsis
Q41805 zea mays (m
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8.5	8.8	8.8	8.9	8. 9	8.9	9.0	9.1	9.2	9.2	9.3	9.3	9.3	9.3	9.3	9.3	9.4	9.4	9.5	9.5	9.6	9.6	9.7	9.8	9.8	9.8
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Best Local Similarity 90.5%;
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PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00120; HX; 2.
SMART; SM000201; SO; 2.
SEQUENCE 1404 AA; 151090 MW; AABD7AI
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180	121 PPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSSTIR	ф
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	PT	Qy Db
25 60	1 MAWKTLPIYLLLLLSVFVIQQVSSQ	Qу
sdŧ	y8.5%; Score 6712; DB 4; Length 1404; t Local Similarity 90.2%; Pred. No. 0; ches 1267; Conservative 0; Mismatches 3; Indels 134; Ga	Que Bes Mat
	SEQUENCE FROM N.A.  Wray P.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  EMBL; AL133553; CAC36090.1;  SEQUENCE 1404 AA; 151076 NW; 782A11746B3FDEE5 CRC64;	RA RA DR
	HOMO Saplens (Human). Homo Saplens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;	
	11-JUN-2001 (TrEMBLrel. 17, Created) 21-JUN-2001 (TrEMBLrel. 17, Last sequence update) 21-JUN-2001 (TrEMBLrel. 17, Last annotation update) 201-JUN-2001 (TrEMBLrel. 17, Last annotation update) 8617416.2 (MSF: MEGAKARYOCYTE STIMULATING FACTOR ).	
	T 2 9 9 99BX49 PRELIMINARY; PRT; 1404 AA.	8 9
	1247 PSRTARAITTRSGQTLSKVWYNCP 1270 	Qy 1 Db 1
1246 1380	187 SPARLAYODKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPOGYDYYAESKDOYYNIDV 	Qy 1 Db 1
32	127 FFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRPERAIGPSQTHTIRIQY	Qy 1 Db 1
126	067 RCNCEGKTEFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESYY	Qy 1 Db 1
.20	007 DETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRITEVMGIPSPIDTVFT	Qy 1 Db 1
14	947 QTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVEMPEVTPDMDYLPRVENQGIIINPMLS 	Ωy Db 1
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                                                      RCNCEGKTFFFKDSQYWRFTNDIKDAGYPKPIFKGFGGLTGQIVAALSTAKYKNWPESVY
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Best Local Similarity 49.7%
Matches 701; Conservative
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InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001212; Somatomedin_B.
InterPro; IPR001212; Somatomedin_B.; 2.
Pfam; PF01033; Somatomedin_B.; 2.
PRINTS; PR010217; PRICHEXTENSN.
PRINTS; PR00021; SOMATOMEDINB.
SMART; SM00110; HX; 2.
SMART; SM00120; SO; 2.
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a novel mouse gene highly homologous to a human
megakaryocyte stimulating factor precursor and ca
zone protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
SEQUENCE 1054 AA; 115991 MW; 4FC64B
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last sequence update)
01-UNY-2001 (TREMBLREL 17, Last annotation update)
RNA, COMPLETE CDS, SIMILAR TO MEGAKARYOCYTE STIMULATING
PRECURSOR AND CARTILAGE SUPERFICIAL ZONE PROTEIN.
                                                                                                               181
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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SKVATSPKTTAAKPVTPKPSLAPNSETSKEASLASNKETTVETKETTATNKQSSA-SKKK
                            NKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEK
                                                                                             SKNSANRELQKNPNVKDNKKNTPKKKPNPEPPAVDEAGSGLDNGEFKLTPPPPDPPTTPH
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                                                                                                                            -VKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVT--TPDTSTTQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 3369; DB 11;
; Pred. No. 2e-218;
54; Mismatches 158;
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Sciurognathi; Muridae; Murinae; Mus
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229 299

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                           TFRIHYSVPMRVSYQDKGFLHNEVKVSTMWRGFPNVVTSAITLPNIRKPDGYDYYAFSKD
                                    TIRIQYS-PARLAYQDKGVLHNEVKVSILWRGLPNVVTSAISLPNIRKPDGYDYYAFSKD
                                                                        WPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFERAIGPSOTH 1180
                                                                                                  TTTIPKQTPNPETAEVNPDHEDADGGEGEKP-LIPGPPVLFPTAIPGTDLLAGRLNRGIN
                                                                                                                                                                                                              QYYNIDVPSRTARAITTRSGQTLSKVWYNCP
                                                               RPESVYFFKRGGNIQQYTYKQEPMKKCTGRRPAINYSVYGEAAQVRRRRFERAVGPFQTH
-TTLKATTLAPKVTAPAE-----EIQNKPEETTPASEDSDDSKTTLKPQKP
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RESULT
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AC QS
DT QS
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Q9N4S7 Q9N4S7; 01-OCT-2000 01-OCT-2000

PRELIMINARY; (TrEMBLrel. (TrEMBLrel.

15, 15,

Created)

sequence update)

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RESULT
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Best Local Sim
Matches 320;
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EMBL; AF056218; AAD13404.1; -.
InterPro; IPR000585; Hemopexin.
Pfam; PF00045; Hemopexin; 2.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
SMART; SM00110; HX; 2.
NON_TER 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aydelotte M.B.;
"Immunodetection and Partial cDNA Sequence of the Proteoglycan,
Superficial Zone Protein, Synthesized by Cells Lining Synovial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-ARTICULAR CARTILA Schumacher B.L., Hughes
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                                                                                                                                                                                                     ALSIAQYKSRPESVYFFKRGGSVQQYTYKQEPTQKCTGRRPAINYSVYGETAQVRRRRFE
                                                                                                                                                                                                                                ALSTAKYKNWPESVYFFKRGGSIQQYIYKQEPVQKCPGRRPALNYPVYGEMTQVRRRRFE
                                                                                                                                                                                                                                                                                                           401 AA; 44952 MW;
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Hughes C.E., Kuettner K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.1%; Score 1713.5; DB 6
80.2%; Pred. No. 1.3e-107;
tive 24; Mismatches 52;
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01-JUN-2001 (TremBLrel. Y51B11A.1 PROTEIN.

17, Last annotation update)

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Best Local Similarity
Matches 330; Conserv
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EMBL; ACCO6797; AAF60743.1; .
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DBDE3824CF80CA1 CRC64;
                                     472
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STRAIN-BRISTOL N2;
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MEDLINE-99069613; PubMed-9851916;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                      241
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Submitted (MA
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TTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP-APTTPKGTAPTTPKEP
                         PETTSTEP-PSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPE-TTSTESPSSS
                                                                               TPVQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTSTEP----PSSSTTPVQTTTTTA 471
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                                                                                                                                                                                                                                                                                                                                                                                                             ETTSTEP-----PSSSTTPVQTTTTTAPETTSTEAPSSSTTPVQTT-----TTTAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 971.5; DB 5; Length 1079; 29.5%; Pred. No. 2.8e-57; tive 129; Mismatches 481; Indels 177;
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EMBL/GenBank/DDBJ
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MEDLINE=20196006; PubMed=10731132;

STRAIN-BERKELEY;

A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bhandari D., Botshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn R.,

K., Doup L.E., Downes M., K.J., Evangelista C.C., F

Ferriera S.,

R R	20000	GN DE		Q917S1 ID Q	RESULT	В	Qy	DЬ	Qy	Db	Qy	Db	Qy	Вb	Qy	Ф	Qу	Db	Qy	Дb	Qy	р	Qy	Db
SEQUENCE FROM N.A.	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  NCBI_TaxID=7227;	TEIN.	16, Creat	S1 S017S1 PRELIMINARY; PRT; 1049 AA.	III 6	1041YNVPTGLE-IWPEINCEGNKWSYNN 1064	1051 ITEVWGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTN 1087	SSIDLPF	1011ICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARR 1050	937 TEPPSSSTTPVQTTTTTVPCDCSLSYIDRVVYPFTTEWWENKRDIIIQSYDSPRRTAFSF 996	969 -ETPHMLLRPHVEMPEVTPDMDYLPRVPNQGIIINPMLSDETN 1010		RIAEAMLQ	825 PSSSNTPVQTTTTTAPETTSTEPPSSSTSPVQTTTTTAPETTSTEPPSSSTTPVQTTT 882	-KPKDRATNSKATTPKPQKPTKAPKK		AAPKMTKETATTTEKTTESKITATTTQV		736 HKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTT 793					

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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Quan P., Harris M., RA Harris N.L., Harvey D., Hedman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Venter E., Wang X., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y.H., Zhong W., Zhou X., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubhn G.M., Venter J.C.; The EMBL, AE003495, AAG22353 1. -

DR SEQUENCE 1049 AA; 107278 MW; 954DD629E7619671 CRC64;
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                                        KGTTAKPTTLK----PTEGTSAKPTTLKPTEGTTAKPTTLKPTEGTSAKPTTLKPTEGTTA
                                                                                                                TLKPTEGTTAKPTTLKPTKGTKGTSAKPTTLKPTEGTTAKPTTLKPTEGTTAKPTTLKPT
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                                                                                                                                                      -TPEKLAPTTPEKPAPTTPEELAPT--TPEEPTPTTPEEPAPTTPKAAAPN
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Pred. No. 6.1e-55;
        -TTKEPTSTTSDKPA
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                                                                                  -PTTLKEPAPTTP
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            -PTTPKGT
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RA Maris J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liako P., Lai B., McIntosh T.C., McLeod M.P., McPherson D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
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EG:56G7.1 OR CG14796.
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.R.,
RA Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylers R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RN [2] The genome sequence of Drosophila melanogaster.";
RR Cadieu F., Drang G., Tolong W., Elector C.,
RA Cadieu F., Drang G., Tolong W., Elector C.,
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RA Cadieu F., Drang G., Tolong W., Elector C.,
RA Cadieu F., Drang G., Tolong W., Elector C., RA C., Elector C., Turner C., Elector C., Turner C., Elector C., Turner C., Elector C.
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419
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InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; Chitin_bind_2; 2.
PRINTS; PR01217; PRICHETTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AE003421; AAF45644.1; -EMBL; AL031028; CAA19845.2; -E1yBase; FBgn0025390; EG:56G7.1.
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                                                                 PEPTSTEKPITSTPKPSTTTPKTSTVASSTEKTTISSPKPTTEKSTENPTTNSVKTSAL
                                                                                                   PAPTTTKKPAPTAPKEPAPTTPK-ETAPTTPKKLTPTTPEKLAPTTPEKP-----AP
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                                                                                                                                                                                                                                                                                     TSKLSTITOKTTITHKETAATTSTEKPKTTTEKTSTVSTTTKKSTESSPKPTSSTGKPT
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12.5%; Similarity 31.8%; [2]; Conservative 52;	ery Match st Local s tches 362	¥ & O
E FROM N.A.  ACE 1-11;  ACE 1-11;  ALCE 1-11;  Contains a series of the EMBL/GenBank/DDBJ databases.  Contains a series of the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. STRAIN=RACE 1-11; Goernhardt B.; Submitted (APR-199) EMBL; AF061185; AAG SEQUENCE 1489 AA;	RP RA RL DR
chora infestans (Potato late blight fungus). La: stramenopiles; Oomycetes; Pythiales; Pythiaceae; CD=4787;	Phytophthora Eukaryota; st; Eukaryota; st; Phytophthora. NCBI_TaxID=478	ROCOCOS
01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) CYST GERMINATION SPECIFIC ACIDIC REPEAT PROTEIN PRECURSOR. CAR90.	01-MAY-1999 ( 01-MAY-1999 ( 01-MAY-1999 ( CYST GERMINAT CAR90.	GN DT
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                                                                                                                                                                                       VRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP--NQTPNSKLVEVNPKSEDAG
                                                                                                                                                                                                                                                 NKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT-----STKKP-KTMPR 908
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SMART; SM00370; LRR; 3.
SEQUENCE 1315 AA; 134401 MW; 64C97A2A01F0936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stratford S., Barnes W., Golubiewski A., Cotter R., McCormick Hohorst D., Gao M., Showalter A., Bedinger P.A.; "Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF159297; AAD55880.1;
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Zea mays (Maize).
Zea mays (Maize).
Zea mays (Mize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACC clade;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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InterPro; IPR001998; Xylose_isom.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003592; LRR_out.
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                                                                                   PEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT
                                                                                                                 PPQVEKTSPPPAPVSSPPTPKSSPPLAPVSSPPQVEKTSPPPAPVSSPPLEPKPSSPPS
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                             PTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT----
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Pred. No. 2e-4
89; Mismatches
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier I., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 Waterston R.;
            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2
                                                     Waterston R.;
Submitted (JAN-1996)
                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
COSMID F35A5.
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	ATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTE 862  :	MTKETATTTEKTTESKITATTTQVTSTTTQDTTPFK	1150	dg Vy	
	PAAPK 1	TKPDSEAAADPVSGPTSKDPKLSKKAF	1090	) Db	
		VPTTKTPAAT	764	Qy	
	TPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSA-EPTPKALENSPKEPG 763	TPETPPPTTSEVSTPTTTKEPTTIHKSP :	1032	₽ \$	
	:      :  ::  :         EKKTPVLAKKAPAKPRDPSPKKAAPV 1	PPTPVKNEVKKWKPPWEDDDEPAEPVSAPEPEKKTPVLAKKAPAKPRDP-	975	g B	
		APTITKGPTSTTSDKP	669	Qy	
	TAPTTLKEPAPTTPKKPAPKEL 668	KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT	919	Db QY	
	-PTPVKNPVKKW-KPPWEDDDEPTEEVKKPSEPEKKTPVLA 918	PSPKKAEPNSPVVPPTPVKNPV		₽ ₽	
	PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP 620		562	Qy	
	PKE		806	Ф	
		PTT	508	Qy	
	KNPVKKWKPPWEDDDA	H -	751	фd	
			454	Qy	
	PEKK-TPVLAKKAPTKPDSEAAADPVSGPSSKDPKLAKKAPVKPRDDSPMKAVPIKPAPK 750		692	dd .	
			399	Qy	
	APAAVKKPEPISKPKDTAPKKAEPUSPVVP-PTPVKKPAVKKWKPPWEDDDAAKAPVTTPK 60		633	B .5	
	NET TO STATE OF THE STATE OF TH		340	0	
	- PAPITPKEPTPTTPKEPAPTTKEPAPTTPK-EP :		573	B 4	
	PTUAKKTPSLAKKDPAPAKESLKPKADTKAPA	χ ,	299	0 1	
	_	-3 ı		B 1	
		H	265	Q	_
	-TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP 2	E	454	B 4	
	PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP 453		ک 4 د	0 10	
	KAETTTKGPA		175	, Q	
	SPVVPPTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPS 393		334	рь	
	PKITTAKPI-NPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKITSAK 174		116	Оу	
	ΑP		274	Db	
	•	1 KNRTKK-KPTPKPPV	71	Qy	_
л	Score 802; DB 5; Length 1274; Pred. No. 8.2e-46; 2; Mismatches 414; Indels 230; Gans	atch 11.8%; cal Similarity 28.0%; 290; Conservative 10	Query Ma Best Loo Matches	<b>ጀመ</b> Ω	
	; 07F6B0D292C1799F CRC64;	SEQUENCE 1274 AA; 138065 MW;	SEQ	QS	
	EMBL/GenBank/DDBJ databases.		Sub	RL DR	

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Best Local :
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Q9LIE8;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO CELL WALL-PLASMA MEMBRANE LINKER PROTEIN.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidi
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidi
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1194
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TAC and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-COLUMBIA;
Kaneko T., Kato T., (
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 4,251,695 bp covered TAC and BAC clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
445
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                                                                                                                                                                                                                                                                                                                                                                                         TQMPPIATP-PIAKSPVATPPIATPPTATPPITIPPVATPPITTPPIANPPIIMPPIATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPT
                                        TTTKSAPTTTKEPAPTTTKSAPTTPKEP---SPTTTKEPAPTTPKEPAP----TTPKKPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                    SKV--LAKPTPKAETTTKGPALTTPKEPTP--TTP--KEPASTTPKEPTPTTIKSAPTTP
                                                                                                                                                                                          PAKPPVAISPIVT--PPVTPIAQPPVATPPTATPPVATPPIATPPTSKSPISTPPISESP
                                                                                                                                                                                                                                                                                           PVAAPPITNPPISKPPVTTP.
                                                                                                                                                                                                                                                                                                                                        KEPAPTTT----KSAPTTPKEPAPTTT-----
TAT---PPVAKPPVETPPIATPPTAKPPISTPPISKPPVATPPAATPPITTPTPVKPPVA
                                                                                           VATPPTATSPIKTPPPAKPPVATPPIAKSPIATPPTATPPVATPPIEKPPVATPPTTTPP
                                                                                                                                         TTKEPAPTTP-KEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                          - PTTTKSAPTTP - KEPAPTTPKKPAP - - TTPKEPAPTTPKEPTPTTPKEPAP
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EMBL/GenBank/DDBJ databases
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Pred. No. 1.2e
54; Mismatches
                                                                                                                                                                                                                                                                                                PTTTPPIAKPPIATPPISTPPAATPPAATPPITTLP
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01-NOV-1996 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTENSIN-LIKE PROTEIN PRECURSOR.
Zea mays (Maize).
Zea mays (Maize).
Exermatophyta; Magnollophyta; Liliopsida; Poales; Ppanicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q41805;
Q41805;
                            Signal.
SIGNAL
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                                                                                                                                                                                      Rubinstein A.L., Broadwater A.H., Lowrey K., F
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ
EMBL; Z34465; CAA84230.1; -.
Mendel; 14346; Zeama; 2368; 14346.
                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 972
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     SEQUENCE
                                                                                    SMART; SM00370;
                                                                                                                                      InterPro;
                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                STRAIN-B73; TISSUE-POLLEN;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990
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                                                                                                                PF00560; LRR; 3.
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                                                                                                                                      IPR001611; LRR.
IPR003592; LRR_out.
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1188
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                                                                                      LRR; 4.
        AA;
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     27 POTENTIAL.
120980 MW; 2C77C7
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           2C77C7F8D7130149
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P70670;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NASCENT POLYPEFTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE
MUSCLE-SPECIFIC FORM GP220).
  Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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                                                                                                                                                                                                                          KSPPPPAPISSPPPPVKSPPPPAPVS--SPPPPVKSPPPPAPVSSPPPPIKSPPPPAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSSPPPPEVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP---PPVKSPPPPAPVSSPPPPV
                                                                                                                                                                                                                                                                                                                                                                                                 VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA---PKSSPPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                          LKE---PA----PTTPKK----PAPKELAPTTTKE----PTSTTSDKPAPTTPKGTAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPASPPAHVSSPPEVVKPSTP--PA
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        Chordata; (
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29.9%;
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              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-96312450; PubMed-8698236;

X MEDLINE-96312450; PubMed-8698236;

X Yotov W.V., St-Arnaud R.;

Thought of a proline-rich exon con a muscle-specific transcription factor.";

RI Genes Dev. 10:1763-1772(1996).

DR EMBL; U48364; AAB18734.1; -.

DR EMBL; U48363; AAB18732.1; -.

DR EMBL; U48363; AAB18732.1; -.
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Best Local Similarity
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InterPro; IPR002715; NaC.
InterPro; IPR003037; TS-N.
Pfam; PF01849; NAC; 1.
Pfam; PF02094; TS-N; 1.
SEQUENCE 2187 AA; 220599 M
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                             LKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT
                                                   TLVTPSSKKLSQTVGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTT
                                                                                                                                                                                                                                                                                                                                                                                            GVTAMPLEIPSAPQKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APKESSATSSSKRAPKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKGAPAMTSKKAT---EIAASKDVSPSQ--FPKEVPLLQHV---PPTSPPKSPVSDTLSG
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LAE-SPSSPKK-APKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVS
                                                                                                                                                           {\tt VAGPKEASATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS-}
                                                                                                                                                                                                                                                           SPPTPASKGVPVTLTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP-----SPQKIPK
                                                                                                                                                                                                                                                                                          KEPAP-----TTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PA
                                                                                                                                                                                                                                                                                                                            GVIAVSGEISPSPKKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISP
                                                                                                                                                                                                                                                                                                                                                           -----EPSPTTTKEPAPTTPKEPAPTTPKKPAPTT--PKE---------PAPTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPKEPAPTTTKEPAPTT--TKSAPT--------TPKEPAPTTPKK-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTSPPPKGPPATLAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PASTTPKEPTPTTIKSAPTTPKE-PAPTTTKSAPTTPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDGKEKTTSAKETOSIEKTSAKDLAPTSKYLAKPTPKAETTTKGPALTTPKEPTPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSLSPPKAPVAPSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPSPQKTPKSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAPTITKEPTS-----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTT
                                                                                                                           -PEGATTAPVQIPPSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKE
                                                                                                                                                                                                                           PTTPEELAPTTPEEPTPTT-----PEEPAPTTPKAAAPNTPKEPAPTTPKE-PAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                          ---TTPKEPAPTTTKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTAGPKE----TPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290;
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27.6%;
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                                                                                                               RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Ž.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Turner R., Vener E., Wang A.H., Wang Y.,
Nan Yang A., Vener B., Wang A.H., Wang Y.,
Nan Yang A., Vener E., Wang A.H., Wang Y.,
Nan Yang A., Vener B., Weight D., Morey M., Wang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RX MEDLINE-2019606; PubMed-10731132;

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,

RA Harris M.L., Basu A., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bermann B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA German B.P., Barriera S., Dunkov B.C., Dunn P.,

RA German B.P., Borrier J., Guz., Gulart W.M., Glasser K.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.I., Harray D., Heiman T.J., Hernander J. P., Houck J.
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Q9VEL9;
01-MAY-2000
01-MAY-2000
01-JUN-2001
CG4090 PROTE
CG4090.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
        Wang Z.-Y., Wassarman D.A., Weinstock G.M., We Williams S.M., Woodage T., Worley K.C., Wu D., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1745
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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Weissenbach J.,
D., Yang S., Yao Q.A.,
ng G., Zhao Q., Zheng
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            Zheng L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1708
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	654	PKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKE	596	Оy
	595 1697	KEPAPTTPKEPAPTT-PKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPA :       :	544 1638	Qу ДЬ
	543 1637	PTIPKKLIPTIPEKLAPTIPEKPAPTIPEELAPTIPEEPIPIIPEEPAPTTPKAAAPNIP	484 1582	Фу
	483 1581	-EPAPTTPKKPAPTTPKEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETA	433 1524	Фр
	432 1523	TTTKEPAPTTPKTTPK	421 1464	Qу
	420 1463	PAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSP	364 1404	ОУ
	363 1403	TTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTFKEPAPTTPKEPAPTAPKKPAPTTPKE	304 1355	Оу
	303 1354	TTKSAPTTPKEPAP TTKSAPTTPKEPAP TTKSAPTTPKEPAP TTKSAPTTPKEPAP	283 1296	Qу
	282 1295	PTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTT	234 1240	Qу
	1239	DRGGENMVPFSCGPGTVWDAQMQACNHAWAVKECGGIAPPTTSTPTTSR-PTTASTSRPS	209 1181	ДЬ
	1 0	KTSAKDLAPTSKVLAKPTPKAETTTKGP	172 1121	Qy Db
	171 1120	TTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTT ::::::::::::::::::::::::::::::::::	119 1067	Qу
	118 1066	ESFCAEVKD-NKKNRTKKKFTFKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKI :   ::   :   :   :   :   :   :   :   :	60 1013	Qy Db
	59 1012	QVSSQELSCKGRCFESFERGRECDCDAQCKKYDKCCPDY       :   : :   : :     : :	21 953	Qу Дъ
47;	aps	atch 11.1%; Score 756; DB 5; Length 2112; cal Similarity 26.4%; Pred. No. 1.7e-42; 292; Conservative 107; Mismatches 367; Indels 338; Ga	ry M t Lo ches	Que Bes Mat
		Science 287:2185-2195(2000).  EMBL; AE003716; AAF55402.1;  FlyBase; EBgn0038492; CG4090.  InterPro; IPR002557; Chitin_binding.  InterPro; IPR000551; EGF-11ke.  Pfam; PF01007; Chitin_bind_2; 10.  SMARP; SM00494; ChtBD2; 11.  PROSITE; PS00022; EGF-1; 1.  SEQUENCE 2112 AA; 219547 MW; B91018E5551A5D36 CRC64;	Scie EMBL FlyB Inte Inte Pfam SMAR PROS SEQU	RL DR DR DR DR DR SQ
	н.О.,	Zhu X., Smith	Zhen Gibb "The	

B 8	655 PAPTTPKKPAPKELAPITTKGPTSTTSDKPAPTTPKETAPTTPKEPAPT 703	
Ş	704 TPKKDADTTDETDDDTTGEVGTDTTTTTTTTTTTTTTTTTTTTTTT	
g d	14 SGN	
B 5	MTKETATTTEKTTESKITATT 823	
Ş	DT TT	
용 :	TATORTYPE DOED THE TITLATE VITTE KTITTE	
, 5	000 TATPETTTKPPKPETTTIAGEETSTSK	
Ş	884 TPKPQKPTKAPKKPTSTKKPKTMP 907	
Ъ	1919 SPAPSTNTSAPCPETGP 1935	
RESU	LT 15	
850 800	Q9XDH2: PRELIMINARY; PRT; 763 AA.	
33	L-NOV-1999 (TrEMBLrel. 12, Created)	
D,	l-JUN-2001 (Trembtrel, 12, Last sequence update)	
SOE	CODACTER HUCIN HOMOLOG.	
88	cteria; Firmicutes; Actinobacteria	
28	BI_TaxID=1773;	
7 7 7	SEQUENCE FROM N.A.	
282	pitia C., Laclette J	
R	loning and characterization of a new member of the pope family.	
R 23	a useful marker of polymorphism in Mycobacterium bmitted (JUN-1998) to the FMBI (Connection)	
2 2	BL; AF071081; AAD41594.1; -	
S S	terPro; IPR002951; Atrophin. terPro; IPR002965; P rich extenso	
2 X	T C	
3 8 9	Į.	
ő;	SEQUENCE 763 AA; 75034 MW; 39168EC45A5916F8 CRC64;	
Que Bes Mat	ry Match 10.5%; Score 715; DB 2; Length 763; t Local Similarity 28.2%; Pred. No. 3.4e-40; ches 248; Conservative 39; Mismatches 361; Indels 737. Gang 20.	
¥	TTIKSAPTTPKEPAPTTTKSAP 256	
ŏ	3 PVPAPRALAPLPPAPPAPAEPKSKPPFPPAPPAPPCWMLVSAAP 46	
ŕ¥	257 TTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 316	
	FEAD	
¥	317 PAPTTPKEPTPTTPKEPAPTTKEPAPTTPK-EPAPTAPK-KPAPTTPKEPAPTTPK 370	
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¥	371 EPAPTITKEPSPITPKEPAPTITKSAPITTKEPAPTITKSAPITPKEPSPITTKEPAP 428	
ъ	APPAPPLANSPPLPPAPPTPAGTPPAAPWPPVPAAPKSKPA 20	
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Search completed: April 26, 2002, 16:29:32 Job time: 587 sec

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OM protein - protein search, using sw model
                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run April 26, 2002, 16:20:05; Search time 114.61 Seconds

(without alignments)
816.844 Million cell updates/sec

Title: Perfect score:

Sequence: MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1229

Scoring table:

Searched:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 219241

219241 seqs, 76174552 residues

Minimum Maximum DB 0 seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database PIR\_68:\* pir1:\*

pir2;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

mucin intestinal human (fragments)

N; Alternate names: mucin SMUC-41

C; Species: Homo sapiens (man

C;Date: 10-Mar-1993 #sequence\_revision 12-Apr-1996 #text\_change 05-Nov-1999 C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.

J. Biol. Chem. 269, 2440-2446, 1994
A; Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification A; Reference number: A49963; MUID:94132002 of.

Accession: A49963

A; Molecule type: mRNA A; Residues: 1-639 <GU1>

E.M.; Lagace, R.E.; Kim, Y.S.

J. Biol. Chem. 267, 21375-21383, 1992
A;Fitle: The human MUC2 intestinal mucin has cystelne A;Reference number: A45106; MUID:93016075
A;Status. ... cysteine-rich subdomains located both up

A; Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 626-1895 <GU2>

A;Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; A;Note: sequence extracted from NCBI backbone (NCBIP:116706) PID:g186396

A; Accession: B45106

A; Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 2037-3020 <GU3>

A; Experimental source: colon A;Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398

A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, J. Ciin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym A;Reference number: A43932; MUID:91358717
A;Recession: A43932

A;Molecule type: DNA
A;Residues: 1343-1350, 'L', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
A;Residues: 1343-1350, 'L', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
A;Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
A;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
A;Reference number: A33532; MUID:89197956
A;Accession: B33532 evi

A;Molecule type: mRNA A;Residues: 1916-2193 <GU4> A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874 A; Experimental source:

B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

A; Ti A; Ti A; Re A; St A; St	ttle: ttle: eferen cessi atus: blecul sidue	J. Clin. Invest. 87, 77-82, 1991 A;Title: Human bronchus and intestine express the same mucin gene. A;Reference number: A61257; MUID:91086481 A;Accession: A61257 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 'T',1925-1948,'TTS',1952-1954 <jan> A:Residues: 'T',1925-1948,'TTS',1952-1954 <jan></jan></jan>
R; Xu Bioc A; Ti A; Re	hem. tle: feren	;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, siochem. Biophys. Res. Commun. 183, 821-828, 1992 ;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t, Reference number: PQ0328; MUID:92198477
A; Ac A; Mo A; Re	; Accession ; Molecule ; Residues	ion: PQ0328  le type: mRNA  es: 2328-2468 <xug></xug>
	oss-r perim	
** ** **	;Molecule t ;Residues: ;Genetics:	e type: protein s: 2328-2342,'K',2344-2354 <xug1> s:</xug1>
A;Ge	Gene: G	GDB:MUC2 -references: GDB:120203; OMIM:158370
A; Ma C; Su C; Ke F; 27	p pos perfa yword 66-28	; Map position: 11p15.5-11p15.5  ; Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von ; Reywords: glycoprotein; intestine; tandem repeat ; 2766-2834/Domain: von Willebrand factor type C repeat homology < VWC>
<u>-</u>	Prv M	16 0%. coore 1060 s. Da
Ве Ма	Best Loc Matches	cal Similarity 29.2%; Pred. No. 8.3e-40; 342; Conservative 74; Mismatches 442; Indels
Qy	56	SDTSKETSLTVNKETTVETK 112
Db	1240	TSFTTTTTTTTPTS
P 68	113	ETTITUKQTSTDGKEKTTSAKETQSIEKTSAKD 145    :
Ş	146	
Db	1352	KVQCDVSVGFICKNEDQFGNGPFGLCYDYKIRVNCCWPMDKCITTPSPPTTTPSPPPTT
Qy	162	TTTKGPALTTPKEPTPTTTPKEPASTTPKEPTPTTIKSAP-TTPKEPAPTTTKSAPTTPKE 220
ДЪ	1412	TTTTLPPTTTPSPPTTTTPPPTTTPSPPITTTTTPLPTTTPSPPISTTTPPPTTTPS 1471
ρh	221	PAPITIKEPAPTIPKEPAPTITKEPAPTITKSAP-TIPKEPAPTTPKEPAPTIPKEPAPT 279
ð	280	
Db. Qy	280 1530	TPKEPTPTTPKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEP 339
ДУ	340 1589	SPTTPKEPAPTTTKSAP-TTTKEPAPTTTKSAP-TTPKEPSPTTTKEPAPTTPKEPAPTT 397
Qy	398	별
Dβ	1649	TTPPPTTTPSPPTTTTPSPPTTTTPPPTTTPSSPITTTPSPPTTTWTTPS 1700
Qу	458 1701	APTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT 517
P 29	518 1760	PKEPAPTTPKETAPTTPKGKG

325	267 KPAPTTPKEPAPTTPKEPAPTTPKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP	Qy	
266 864	211 TKSAPITPKEPAPITIKEPAPTTPKEPAPITIKEPAPITIKSAPITPKEPAPTTPK :   :	Qy	
210 804	152 VLAKPTP-KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPAPTT IKSAPTTPKEPAPTT	Qy	
ps 55;	14.5%; Score 950; DB 2; Length 1664; Best Local Similarity 31.0%; Pred. No. 4.4e-35; Matches 312; Conservative 104; Mismatches 361; Indels 230; Ga	Que Bes Mat	
<del>1</del>	Reference number: Z18847; MUID:93209931 Accession: T18262 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 1-1664 <fuj> Cross-references: EMBL:X67506; NID:g296879; PID:g296881; PIDN:CAA4784</fuj>	** ** ** ** ** ** *	
ing the cellulo	bert, J.P. , 1993 lostridium thermocellum gene cluster encod	R; Fuj	
-1999	RESULT 2 T18262 S-layer protein - Clostridium thermocellum C;Species: Clostridium thermocellum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct C;Accession: T18262	RESUI T1826 S-lay C; Spe C; Dat	
	935RPHVFWDEVTPDMDYLPRVPNOGIIIN 961 :  :  :  :        :  :	рь	
934 2337	905 NQTPNSKLVEVNPKSEDAGGAEGETPHMLL	ОУ	
904	845 KPQKPTKAPKKPTSTKKPKIMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTITRP	Оy	
844 2232	814 KKTITTTEIMNKPEETAKPKDRATNSKATTP :	Qy	
813 2173	757 TAAPKMIKETATTIEKITESKITATTIQVTSTTTQDTTPFKITTLKTITLAPKVTTT	Qy Db	
756 2115	697 SPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETT	Оу	
696 2055	649 KETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHK	Db Qy	
648 1995	590 PAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTST-TSDKPAPTTP	Ду	
589 1936	537 TAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT-TPKGTAPTTPKE	Ωу	
1879	1820 NISCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQKPGGVIPMAFCLNYEINVQCCECV	Db	
536	537	Qy	

C;Genetics: A;Gene: car90

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cyst germination specific acidic repeat protein precursor - Phytophthora infestans (Species: Phytophthora infestans (potato late blight agent) C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C:Accession: T31108 R:Goernhardt, B. submitted to the EMBL Data Library, April 1998 A:Reference number: Z20986 A:Recession: T31108
A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1489 <GOE> A;Cross-references: EMBL:AF061185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLRGYPDGSFRPERNITRAEAAVIF-----AKLL----GADESYGAQSASPYSD
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TTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT---
                                                                 TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTT------PFKITT---LKT
                                                                                                      TEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTEET
                                                                                                                                     AEPTPKA-LENSPKEPG-----VPTTKTPAATKPEMTTTAKDKTTERDLRTTP----ETT
                                                                                                                                                                          YAPAEETPYEPTEETTYAPTEETTYAPTEETMYAPIEETTYGPTEETTY-APTEATTYAP
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                                -TEETTYEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEE
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Db 1285 TIYAPTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETPYE	NPTEETTYAPMEETPYE 1344
QY 858STKKP-KTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTT	TSTMPELNPTSRIAEAMLQTTTRPN 905
Qy 906 QTPNSKLVEVNPKSEDAG 923	
SULT 4 6251 pothetical protein F35A5.1 Species: Caenorhabditis ele	
C;Accession: T16251 R;Leimbach, D. R;Leimbach, D. submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid A;Reference number: Z18485	F35A5.
A; Recidues: 1-1274 <lei>A; Residues: 1-1274 <lei 1-1274="" <<="" <lei="" a;="" residues:="" td=""><td></td></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei></lei>	
Cross-references: EMBL:U46675; NID:g1166613; Cross-references: EMBL:U46675; NID:g1166613; Experimental source: strain Bristol N2; clone; Genetics; Gene: CESP:F35A5.1; Map position: X; Introns: 1272/2	PID:g1166621; PIDN:AAB52641.1; GSPDB:GN0C F35A5
Query Match 12.2%; Score 802; DB Best Local Similarity 28.0%; Pred. No. 1.2e-Matches 290; Conservative 102; Mismatches	Length 1274; Indels 230; Gaps 56;
Qy 30 KNRTKK-KPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTOHNKVSTS	FKVTTPDTSTTOHNKVSTS 74
QY 75 PKITTAKPI-NPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQTSTDGKEKTTSAK :  :	INKQTSTDGKEKTTSAK 133 
QY 134 ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA	
Qy 173 KEPTPTTPKEPASTTPKEPTP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT	TTIKSAPTIPKEPAPTITKSAPTIPKEPAP 223 
Qy 224 TITKEPA	TTKSAPTTP 257
UD SI3 TEVKNEVKKWREEWEUUETEAUUVSKETUAKKTESLAKKUPAPAKESLKEKAUTKAPAKE	KESEKPKADIKAPAKP 5/2
Qy 258 KEPAPTIPKKPAPTIPKEPAPTIPKEPTPTTPKEPAPTTKEPAPTTPK-EP	PAPTTPKEPTPTTPKEPAPTTKEPAPTTPK-EP 307
308	(Li
 633 APAAVKKPEPISKPK	
Qy         358 TIKEPAPITIKSAPITP-KEPSPITIKEPAPITIPKEPAPITIPKKPAPTIPKEPAPI           1	EPAPTTPKKPAPTTPKEPAPT 412
Qy 413 TPKEPAPTTTKKPAPTA-PKEPAPTTPKETAPTTPKKLTPTTP	EKLAPTTPEKPA 466
Db 751 TEVPPAVVKKPEPVAKSRDPSPKKAK-AEPNSPVVPPTPVKNPVKKWKPPWEDDDA	KNPVKKWKPPWEDDDA 805

	ADFTMPAPKKPDTEDP 1259	1244	Db
	TTPTPRKMTSTMP 885	873	Qy
1243	PPKP-AAPKKWKPPWEDDPDEPE	1194	DЬ
872	IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK	822	Qy
1193	KWKPVWDDDPDEPEADETVPAPSKKPDTEDPADPLGGPKTKDPK	1150	DЬ
821	MTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE {	762	Qy
1149	TKPDSEAAADPVSGPTSKDPKLSKKAPVEKPKPTTDPKDDKLKPSPAKKPEKAPEPAAPK	1090	Db
761		723	Qy
1089	AAK-PDPKIPEV-PPTEVKNEVKKWKPPWEDDDEPSEPVSAPEPEKKTEVLAKKAPTKPA	1032	Db
722		671	Qу
1031	PPTPVKNPVKKWKPPWEDDDEPAEPVSAPEPEKKTPVLAKKAPAKPRDPSPKKAAPV	975	Db
670	APTTTKGPTSTTSDKPAPTTPKETAPTTPKKPAPT (	628	Qy
974	-APKVAAKPRDPSPKKAVPEKEPAKVAAKPRDLSPKKAIPIPANTQEA	919	В
627	KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKEL (	580	Qy
918	PSPKKAEPNSPVVPPTPVKNPVKKW-KPPWEDDDEPTEEVKKPSEPEKKTPVLA	866	В
579	APTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP	521	Qy
865	PAEPVNVPEPEKKTPVLAKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKE	806	В
520	PAPTTPKEPAPTT-PKE	467	Qy

glucan 1.4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
W.Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIRO1
; Species: Saccharomyces cerevisiae
C.Date: 10-Sep-1999 #sequence\_revisian
C.Paccession: S48478
R.Rowley, K.

R.Rowley, K.

A.Reference number: \$48478
A.Reference number: \$48478
A.Reference number: \$48478
A.Reference number: \$48478
A.Reference number: \$11367 < Row
A.Coession: \$48478
A.COESSION: \$1242-2142, 1987
A.COESSION: \$1242-2142, 1987
A.COESSION: \$248278
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A.COESSION: \$26877
A.COESSION: \$27281; MUID: \$172523; PIDN: \$4435014.1; PID: \$172526
A.COESSION: \$27281; MUID: \$172523; PIDN: \$4435015.1; PID: \$172526
A.COESSION: \$27281; MUID: \$172523; PIDN: \$4435015.1; PID: \$172526
A.COESSION: \$27281; MUID: \$172523; PIDN: \$4435015.1; PID: \$172526
A.COESSION: \$27281; MUID: \$189031230
A.COESSION: \$27281; MUID: \$189031230
A.COESSION: \$27281; MUID: \$189031230
A.COESSION: \$27281; MUID: \$189031230
A.COESSION: \$27281; MUID: \$24551; PIDN: \$2432069.1; PID: \$24552
A.COESSION: \$27281; MUID: \$24551; PIDN: \$24552
A.COESSION: \$25281

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Cispecias: Zea mays (maize)
Cispecias: Subjective is Subjective in Subje
                                                                                                                                                                                                                                                                                             -SVTIVINFTPTT-ITTTVCSTGT------NSAGETTSGCSPKTVTTTVPCST 1122
                                                                                                                                                                                                                                                                                                                                                                                            1123 GTGEYITEATTLVTTAVTTTVVTTESSTGTNSA-GKTTTGYTTKSVPTT-----YVTTL 1175
                                                                                                                                                                                      ---SESTITSPITPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTTAPTP- 1077
                                   --TTQVTSTTTQDTTPFKITTLKTTTLAPKVTT---TKKTITTT-EIMNKPEETAKPKDR 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 PTPHSPPAD------DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ 510
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                                                                      TKAPKKPTSTKKPKTMPRVRKPKTTPTPR
                                                                                                                                                                                                                                            KMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV
                                                                                                                                                                                                                                                                                                                                              939 FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APVG-----SPAPPVKTTSPPAPIG----SPSPPPVSVV
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29.9%; Pred. No. 7.2e-28;
iive 59; Mismatches 359;
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Best Local Similarity
Matches 230; Conserv
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F;1350-1366/Domain: transmembrane #status predicted <7Ml>
                             critical for pseudohy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                A Title: Mucl, a mucln-like profess that is regulated by Mssl0, is critical A;Reference number: JC6123; MUID:96323237
A;Accession: JC6123
A;Accession: JC6123
A;Accession: JC6123
A;Accession: JC6123
A;Molecule type: DNA
A;Residues: 1-1367 < LAM>
A;Cross-references: GB:U30626; NID:91304386; PIDN:AAC49609.1; PID:91304387
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 TIPDISITQHNKVSISPKITIAKPINP-----RPSLPPNSDISKETSLIVNKETIVE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 LTTPKE-----PTPTTPKEPASTTPKEPTPTTIKSAP----TTPKEPAPTTKSAPTP 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.4%; Pred. No. 4.7e-28;
Matches 301; Conservative 104; Mismatches 483; Indels 171;
Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
                                                                                                                                                                                                                            A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:SO001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
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Db 828 LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPASPPAHVSSPPEVVKPSTPPA 885	qq	1086 ETPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMP 1142
QY 483 PITPEEPAPITPKAAAPNIPKE-PAPITPKEPAPITPKETAPITPKGTAPIT 541	QY	329 KEPAPTITKEPSPITPKEPAPTITKSAPTITKEPAPTIT-KSAPTITF 375 1143 LEIPSAPÇKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASRTAAPKEAPATPSVGVIAVS 1202
QY         542 LKEPAPAPKELAPTTKEPASTTSDKPAPTTPKGTAPTTP 587           :	Qy	376 -EPSPTTTKEPAPTTPKEPAPTT-PKEPAPTTPKEPAP- 419 
QY S88 -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT 646  DD 1001 MSSPPPPEVKSPPPPAPVSSPPPVKSPPPAPVSSPPPPVKSPPPAPVSSPPPV 1057	Qy	420TITKRPAPTAPKEPAPTTPKETAPTTPEKLAPTTPEK-PAPTTPEE 472 
QY 647 -TPKETAPTTPKEPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL 705	QQ	473 LAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKE-PAPTTPKEPAP 523 :     :
OY 706 SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET 755	Qy	524 TTPKETAPTTPKGTAPTTLKEPAPTTP
RESULT 7 T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse N;Alternate names: alpha-NAC protein	Qy Db	564 KEPTSTTSDKPAPTTPKGTAPTTPKE-PAPTTPKCTAPTTLKEPAP 616  1
_change 24-Nov-1999	Db Qy	( APKTAAPPSER-VTTVPPFEKPA-TPQKASGTTASKVPVPAETQEVAV PTTSEVSTPTTKEPTTIHKSPDESTPELSAEPTPKALENSE
CONVELUS alphanac linco a muscr	do do	725 TTKTPAATKPEMTTTAKDKTTERDLRTTPAPKMTKETATTTEKTTESKITATTTO 784 1
A; Residues: 1-2187 <yot> A; Residues: 1-2187 <yot> A; Cross-references: EMBL: U48363; NID: 91666688; PID: 91666689; PIDN: AAB18732.1 C; Genetics: Acceleration A</yot></yot>	Qy Db	785 VTSTTTQDTTPFKITTLAPKVTTTKKTITTTEIMNKPEETAKFORATNSKATTP 844 :
A;Map position: 10 A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Note: differential splicing converts alphaMAC into a tissue-specific DNA-binding activ C;Reywords: alternative splicing; DNA binding; transcription factor	QY Db	845 KPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP 904
Query Match 11.9%; Score 778.5; DB 2; Length 2187; Best Local Similarity 27.9%; Pred. No. 2.4e-27; Matches 292; Conservative 119; Mismatches 420; Indels 215; Gaps 48;	Qy	905 NQTPNSKLVEVNPKSEDAGGAEGETP 930   :     :
QY 22 VSSVKDNKKNTTKKRPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPK 76	RE: A3:	RESULT 8 A35175 Mucin   precursor, repetitive splice form A [validated] - human
Qy 77 ITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEK 128		. 2
Qy 129 TISAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTP 188                ::   ::      :	0025	C, Date: 10 Api - 200 Api
Qy 189 KEPTPTIKSAPTTPKE-PAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPA 238	AAA	Acference number: A35175; MUID:90202794 Accession: A35175; MUID:90202794 Accession: A35175
Qy 239 PTTTKEPAPTTTKSAPTTRAPTTREPAPTTPKK-PAPTTPK 274  :::    :	4444	residues: 1-927,1033-1043, 38.505288; NID:9182121; PIDN:AAA35804.1; PID:9182124; Cross-references: GB.M32738; GB.J05288; NID:9182121; PIDN:AAA35804.1; PID:9182124; Experimental source: splice form A Experimental source: splice form A NOTE: GenBank entries HUMEPISIAl and HUMEPISIA2 present only the amino-and carboxyl Note: GenBank entries HUMEPISIA1 and HUMEPISIA2 present only the amino-and carboxyl
Qy 275 EPAPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTP 328	A A A	A;Accession: Boil) A;Molecule type: mRNA A;Residues: 1-19,29-952,1033-1344 <lig2></lig2>

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                                                                                                                                   A.Cross-references: GB:M32739; GB:J05288; NID:9182126; PIDN:AAA35806.1; PID:9182129; GB: A.Experimental source: splice form B A:Rxperimental source: splice form B A:Note: GenBank entries HUMED:SIB1 and HUMEDISIB2 present only the amino-and carboxyl-en R:Gendler, S.J.; Lancaster, C.A.; Taylor-Papadimitriou, J.; Duhig, T.; Peat, N.; Burchel A:Title: Molecular cloning and expression of human tumor-associated polymorphic epitheli A:Reference number: A35886; MUID:90368715 A:Recession: A3886 A:Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region and C; Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c partial repeats. The repeat shown is defined by Smai nuclease sites.
C; Comment: Serine and threonine residues in the tandem repeat domain are extensively gly C; Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48146
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A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057 <MAS>
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057 <MAS>
A; Experimental source: gastric carcinoma cell
R; Zithan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.
FEBS Lett. 356, 130-136, 1994
A; Title: Tyrosine phosphorylation of the MUCI breast cancer membrane proteins cytokine
A; Reference number: S51026; MUID:95080414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Gene: GDB:MUC1; PUM
A:Cross-references: GDB:120705; OMIM:158340
A;Map position: 1q21-1q23
A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
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F;1-23/Domain: signal sequence #link PREA #status predicted <SIGA>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-31344/Product: mucin i precursor, splithelial tumor antigen splice from F;138-1017/Region: 20-residue repeats (GSTAPPAHGVTSAPDTRPAP)
F;1384-1017/Region: aucin i carboxyl-terminal non-repetitive
F;143-127/Domain: transmembrane #status predicted <TRM>
F;144-1272/Domain: transmembrane #status predicted <TRM>
F;144-1373/Domain: transmembrane #status (GSTAPPAHGVTSAPDTRPAP)
F;1213/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                 101 LTVNKETTVETKETTTTNK--QTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP-----KKPAPTTPKEP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 ISAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 TSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKSAPTTPKEPSPTTTKEP-----APTTPKEPAPTTPK----KPAPTTPKEPAPTTPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGVTSAPDTRPAPGSTAP----PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTPTT-----IKSAPTTPKEPAPTT-----KSAPTTPKEPAPTTKEP-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --APTTPKEPTPTTP-----KEPAPTTKEP-----APTTPKEPAPTAPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPAPTTPKEPAPTTPK -- - - EPAPTTKEPSPTTPKEPAPTT - - - TKSAPTTKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657 KEPAPTTP------KKPAPTTPETPPPTTSEVSTPTTTKEPTT-----IHKSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 ESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----TKPEMTTTAKDK---TTERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ELAPITPEEPTPTTP-----EEPAP--TTPKA----AAPNTPKEPAPITPK-
                                                                                                                                                                                                                                                                                                                                                                      Indels 256;
                                                                                                                                                                                                                                                                                                                  Length 1344;
                                                                                                                                                                                                                                                                                                         10.2%; Score 672; DB 1; L
llarity 27.8%; Pred. No. 7.6e-23;
Conservative 78; Mismatches 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   =
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                                                                                                                                                                                                                                                                                                                                                             310;
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                         Local
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Matches
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AAAKLLG  SAAGGNG  SAAGGNG  TO THE STANDARD SPITTKGP  NTMQVSP  NTTMQVSP  NTTTOPP	OY 636TSTTSDKP-APTTPKETAPTTPKKP-APTTPETPP 676	1078 914 1105	RESULT 10 725697 hypothetical protein F16F9.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: T25697 C; Accession: T25697 R; Fulton, B submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmid F16F9. A; Reference number: Z2007 A; Reference number	A; Molecule type: DNA A; Molecule type: DNA A; Moss-references: 1-1229 <ful> A; Cross-references: EMBL: U6/956; PIDN: AAB07691.1; GSPDB: GN00028; CESP:F16F9 A; Experimental source: strain Bristol N2; clone F16F9 C; Genetics: A; Map position: X A; Map position: X A; Introns: 35/1; 361/1; 384/1; 482/2; 517/1; 971/1; 1021/2; 1179/3</ful>	Query Match  Query Match  10.0%; Score 659.5; DB 2; Length 1229;  Best Local Similarity 29.0%; Pred. No. 2.5e-22;  Matches 307; Conservative 78; Mismatches 339; Indels 333; Gaps  Qy 57 KVTT-PDTSTTQHNKVSTSPKITTA-KPINPRSLEPRNSDTSKETSLTVN 104
Db 833 TRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVT 888  Qy 800 TLKTTTLAPKVTTTKTTTTEIMNKPEETAKPKDRATUSKATTPKPQKPTKAPKKPT 857  Db 889 SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHG 946  Qy 858 STKKPKTMPRVRKPKTTTPTPRKMTSTMPELNPTSRIAEAMLQT-TTRPNQTPN 909  Qy 910 SKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPAMDYLPRVPOMDTLINPMLSDETN 969  Qy 910 SKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPAMDYLPRVPAGSTAPPVHNVTS 1049  Qy 970 ICNGKPVDGLTTLENGTLVAFRGHYFWMLSPFSPPS 1005  Db 1050 ASGSASGSASTLVHNGTSARATTPASKSTPFSIPS 1085	RESULT 9 T18535 high molecular mass nuclear antigen - chicken (fragment) C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Species: Gallus gallus C;Dact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18535 R;Shimada, K.; Harata, M.; Mizuno, S. J. Cell Sci. 110, 3031-3041, 1997 A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick A;Reference number: Z18955; MUID:9803440 A;Title: A nuclear matrix-associated from GB/EMBL/DDBJ A;Title: A nuclear matrix-associated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1151 <shi>A;Residues: 1-1151 <shi>A;Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1</shi></shi>	Query Match 10.2%; Score 671; DB 2; Length 1151; Best Local Similarity 25.9%; Pred. No. 7.2e-23; Matches 284; Conservative 100; Mismatches 419; Indels 292; Gaps 55; Qy 38 TPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 88	QY         89 LPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDL 146           b         171ASAASPTVEKATABEATAVTAASQSAPKAATDAAAVTAASQSAPKATV-EV 219           QY         147 APTSKVLAKPTPKAETTTKGPALTTPKEPTP-TTPKEPASTTPKEPTPTTIKSAPT 201           D         220 KPAAAVAKEAKAVTAAAAAPKATAARAKPAPYTSPTIPCSSAEAKPLTAASPTASKA-T 277           QY         202 TPKEPAPTTTKSAPTTPKEAPTTTK	228 EPAPTTPKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPK	OY 331 PAPTITKEPSPTITKSAPTITKEPAPTITKSAPTITKE 384    1

C; Accession: 138346
R; Labeit, S.; Kolmerer, B.
Schence 200, 233-296, 1995
A; Reference number: A57430; MUID:96026330
A; Recession: 138346
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-7962 <RES>
A; Cross-references: EMBL:X90569; NID:91017426; PIDN:CAA62189.1; PID:91017427
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Map position: 2q31-2q31 61; C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000 6045 5874 VSKKIVPQKPSRTPVQEEVIEVKVPAVHTKKMVISEEKMFFASHTEEEVSVTVPEVQKEI 5933 6099 PVPEEKVAVPVPVAKKAPPPRAEVSKKTVVEEKRFVAEEKLSFAVPORVEVTRHEVSAEE 6158 11 | 1: 6159 EWSYSEEEEGVSISVYREEEREEEREAEVTEYEVMEEPEEVVVEEKLHIISKRVEAEPAE 6218 6219 VTERQEKKIVLKPKIPAKIEEPPPAKVPEAPKKIVPEKKVPAPVPKKEKVPPPKVPEEPK 6278 -----TPDTSTTQHNKVSTS-PKITTAKPINPRPSLPPNSDTSKETSLT---VNKET 107 :1 6339 EEKVLKLKPKREEEPPAKVTEFRKRVVKEEKVSIĖAPKREPQPIKEVTIMEEKERAYTLE 6398 6399 EEAVSVQREEEYEEYEEYEEYEEYEEYEPTEEYDQYEEYEEREYERYEEHBEYITEPEKPI 6458 Gaps 331 18 VIQQVSSVKDNKKNR-----TKKKPTP----KPPV---VDEAGSGLDNGDFKVT---- 59 ------EPAP 301 395 402 6515 KIHISITKREKEQVTEP---AAKVPMKPKRVVAEEKVFVPRKEVAPPVRVPEVPKEEPE 6571 PT--TPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEK---- 456 ---LAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP--NTPKEPAPTTPK 511 TVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPT -- SKVLAKPTPKAETTTK 166 GPALTTPKEPTPTTPKEPAS----TTPKEPTPTIKSAPTTPKEPAP-----209 ITIKSAPITPKEPAPITIKEPA-PITPKEPAPITIKEPAPITIKSAPITPKEPAPITPKK 332 APTITKEPSPTTPKE----PAPTTTKSAPTTTKEP--APTTTKSAP---TTPKEPSPTTT TT-----PKEPA-----PTAPKK-----PAPTTPKE--PAPTTPKEP-11arity 22.8%; Pred. No. 2e-20; Conservative 106; Mismatches 463; Indels 444; PAPTTP-KEPAPTTPKEPTPTT-------------PKEPAPTTK-----Query Match Best Local Similarity Matches 300; Conserv 108 09 268 302 289 6459 396 403 457 à ò g ò g ò g 셤 ò q ò ö g ò qq g õ οy QQ qq õ

Gaps

44;

Indels

252;

33;

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Conservative
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Best Local Simil
Matches 217; C
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A;Map position: 2
 149;
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A;Cross-references: EMBL:X91836; NID:g1015936; PIDN:CAA62943.1; PID:g1015937
A;Experimental source: Sub_species de calcalone, W.J.; Krause, A.
B;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
Submitted to the EMBL Data Library, April 1995
A;Description: A class of root-hair specific extensins involved in rhizobium/legume inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cypea

extensin class 1 precursor - cowpea

cyspecies: Vigna unguiculata (cowpea)

cyspecies: Vigna unguiculata (cowpea)

cyspecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000

cyspecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000

cyspecies: The Comparation of States 17-Nov-2000

A; Title: Rhizobia modulate rock-hair specific expression of extensin genes.

A; Reference number: 217301; MUID:97155574

A; Recession: T1622

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-489 *cARS>
                                                                                                                                                                                                                                                                                                                                                                                  6854 EIKKKVTEKKVVIPKKEEAPPAKVPEVPKVE--EKRIILPK----EEEVLPVEVTEEPE 6907
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6740 TPVPKKVEAPPPKVPKKREPVPVPVALPQEEEVLFEEEIVPEEEVLPEEEEVLPE-EEEV 6798
                                                                                                                                                                               6572 EVAFEEEVVTHVEEYLVEEEEEYIHEBEEFITEEEVVPVIPVK-VPEVPRKPVPEE-KKP 6629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 KMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV 938
                                                                                                                                                           653
                                                                                                                                                                                                                                                                                                                                                              768 ITTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPE 827
                                                                                                                                                                                                                                                                                                                                                                                                                                   878
                                                                                                                                                                                                                                                                                             TPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDL--RTTPETTTAAPKMTKETA 767
                       PTTPKEPAPTTPKETAPTTPKGTAPTTLKEP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                 ETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKK-----PKTMPRVRK---PKT-TPTPR
                                                                                                              PTTPKGTAPTTLKEPA--PTTPKKPAPKEL----APTTTKGPTSTTSDKPAPTTPKETAP
                                                                                                                                                                                                                                                                                                                     546 APTTPKKPAPKELAPTTTKEPTSTT-----SDKPAPTTPKGTAPTTPKEPAPTTPKEPA
                                                                                                                                                                                                                            T-TPKE---PAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- PKKVPEKKVL--VPKKEAV-------PPAKGRIVLEEKVSVAFR 7021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFR 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Ext26G
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
C;T-23,Domain: signal sequence #status predicted <SIG>
F;1-23,Domain: extensin class 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 326-489 <AR2>
A;Cross-references: EMBL:X86030; NID:g791149; PID:g791150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 633; DB 2;
Pred. No. 1.5e-21;
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9.6%;

Query Match Best Local Similarity

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hypothetical protein At2927380 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84672
C;Accession: C84672
K;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 KSAPTTPKEPAPTTTKEPAP--TTPKEPAPTTTKEPAPTTTKSAPTTP----KEPAPT-- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 PTPKABITTKGPALTTP---KEPTPT-TPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PITIKEPISITSDKPAPITPKGTAPITPKEPAPITPKEPAPITPKGTAPITLKEPAPITP 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KSPPPPSPSPSPPPYYKKSPPPPSPSPPPPYYYKSPPPPSPPSPPSP 422
                                                                                                                                                                                                                                                                                                                                                                                        ETAPITPKKLIPTTPEKLAPITPEKPAPTTPEELAPITPEEPTPTTPEEPAPTTPKAAAP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                        307
                                                                                                                                                                                                                                           PKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAP 262
                                                                                                                        TIPKKPAPTIPKEPAPTIPKEPIPTIPKEPAPTIKEPAPTIP---KEPAPTAPKKPAPTT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 KKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPP 677
                                                                                                                                                      PKEPAPITPKEPAPITIKEPSPITPKEPAPITIKSAPITIKEPAPITIKSAPITPKEPSP
                                                                                                                                                                                                                                                                                                      380 TITKEPAPITPKEPAPITPKKPAPITPKEPAPITPKEPAPITTKKPAPIAPKEPAPITPK
                                                                                                                                                                                                                                                                                                                                                                                                                     PKQTPPYYYNAPPYYYKSPPP-----PSPSPP-----PPPYVHKYPPYYYKSPPP
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31.1%; Pred. No. 2.5e-21;
ive 44; Mismatches 354; Indels b
Mismatches
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A, Cross-references: GB:4
C; Genetics:
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DD 242  QY 370  DD 302  QY 425  DD 361  DY 472  DD 481  DY 472  DD 533  DD 532  DD 533  DD 533		) APTTPKEPSPITTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKK 424  :   :	PAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPE	ELAPTIPEEPTPTEEPATTTPKAAAP-NIPKEPAPTITPKEPAPTITP	TYSPPVQPPPVQKPPTYSPPVKPPPLQKPPTPTYSPPVKPPTYTY	TIPKEPAPITPKEPAPI-TPKGTAPITLKEPAPITPKKPAPKELAPITTKGPISTISD 6			Δ .	APKMTKETATTEKTTESKTTESTUSTUSTESPOVOLDD-		RESULT 14 174513 hypothetical protein ZK783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34513 R;Favello, A, Vaudin, M. submitted to the EMBL Data Library, August 1994 A;Pescription: The sequence of C. elegans cosmid ZK783. A;Accession: T34513	preliminary; translated from GB/EMBL/DDBJ type: DNA	nesidues: 1-330/ crAV> Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1 Experimental source: strain Bristol N2; clone ZK783 Genetics:	SP:2K783.1 tion: 3 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2;	Match 9.6%; Score 629; DB 2; Length 3507; Local Similarity 24.1%; Pred. No. 1.6e-20; Less 252; Conservative 158; Mismatches 416; Indels 218; Gaps 45;	TSPKITTAK 81	PINPRPSLPPNSDTSKETSLTVNKETTV-ETKETTTTNKQTSTDGKEKTTSAKETQS 137	DMTSSKS-PENVTMSSESPEVSTSSSKSTTASETTVSSTPSESSSEAPLTSSPATTTEV 2060
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2179 ASVAPVKLSSLSPDVSQPSTKTFDATESSTVQASETSSGTSVKSTSEPESHVTKLSITSS 2238 2350 NLSQSSTVSTEDRSEISSENSEKPT-SAPELVTSSVTHVASSSPDVPTES--SEPDDLTG 2406 2407 SSTENIPEASSKQTISSTPTPDTTTASEEPTKSTSMSPDLSTTSNVLSESSTTPESSS-- 2464 421 -----TKKPAPTAPK------EPAPTTPKETAPTTPKKLTP 451 534 2703 SGSLESSTMSSTG-----SEPETNAPAVTVSSEASSTTLEENSSTSSP----TSSEASV 2752 2753 KLSSLFPESITSEAVTVSSR----APABIIMSSESHREISTVSSEPSEPEIPLSTTVSPN 2808 618 TPKKPAPKELAPTTTKGPT-STTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPP 676 617 677 PTISEVSTPTITKEPTIIHKSPDESTP--ELSAEPTPKALE--NSPKEPGVPTTKTPAAT 732 783 -----QVTSTTTQDTTP-FKITT-----LKTTTLAPKVTTTKKTITTEIMNKP 826 827 EETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK---TTPTPRKMTST 883 194 ITIKS-APTIPKEPAPTITKSAPTIPKEPAPTITKEPAPTIPKEPAPTITKEPAPTITKS 253 APTTPKEPAPTTPKKPAPTTPK-EPAPTTPKEPTPTFKEPAPTTKEP-APTTPKEPAPT 311 APKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTP--KEPAPTTTKSAPTTTKEPAPTTTK TTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEP-----APTTPKAAAPN 369 SAP-----TTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT-501 TPKEPAPTT----TPKEPAPT-----TPKEPAP----TTPKETAPTTP 2465 --KSPVSSSTEGISVVTSTEFSKVPESTISSVLEEDLTKTTPSPILEETTTASETSEPLT 535 KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPA------PT----------TP--KGTAP--TTPK-----EPAPTTPKEPAPTTPKCTAPTTLKEPAPT 733 K----PEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT----2809 VVTASSIPSEEDILSSVTSSSTPRVRLITGTFDDLIVSVTVPSHGNRRQNITASSV---P 2919 PPPSNGGYGEETNQEEEQVISTTT 2942 884 MPELN-----PTSRIAEAMLQTTT 902 452 422 578 784 RESULT 15 ò g g ò qq ò ò Ω ò qq δ g δ qq qq δ ò g q ò ò q g δý δ ద δ

RESULT 15
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nucleolar phosphoprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 \*\*sequence\_revision 13-Sep-1996 \*\*text\_change 24-Sep-1999
C;Accession: 151618; S5777
R;Cairns, C.; McStay, B.
J. Cell Sci. 108, 3339-3347, 1995
A;Title: Identification and cDNA cloning of a Xenopus nucleolar phosphoprotein, xNopp

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A;Reference number: 151618; MUID:96019267
A.Accession: 151618
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: 1-990 <CADA
A;Residues: 1-990 <CADA
A;Residues: 1-990 <CADA
A;Coss references: EMBL:X88927; NID:9895920; PIDN:CAA61368.1; PID:9895921
C;Genetics:
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C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
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9.5%; Score 627; DB 2; Length 990;
Best Local Similarity 26.2%; Pred. No. 5.5e-21;
Matches 258; Conservative 134; Mismatches 401; Indels 192;
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

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AA1 6568 1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1229 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		002817 homo sapien	Q06852 clostridium	0		mortilus ed	homo san	_			-	_	xenopus	homo sap	_		-			zea	mus musch		P37370 saccharomyc	P48634 homo sapien	••	•			hômo sar		herpes s	schizos		mus m
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	Score	1168	950	789.5	651	526.5	555.5	551	533	530.5	230	910	509.5	503.5	498.5	497	493.5	488.5	488	475.5	471.5	468.5	467	463	40.0	404	0.00	442.5	439.5	432.5	432	426.5	42	424.5
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### ALIGNMENTS

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1397 SGGSGGGGGGGGGGTVPISPTPISKPISTPAP---TEIEEPIPSDVPGAIGGEHRA 1453
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                                                                                                                                                                                                                                       rry Match
t Local Similarity 31.0%; Pred. No. 2.7e-32;
ches 312; Conservative 104; Mismatches 361; Indels 230;
     POTENTIAL.
CELL SURFACE GLYCOPROTEIN 1.
4 X 156 AA APPROXIMATE REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
Pardo J.M., Ianez E., Zalacain M., Claros of the STA2 and SGA genes
from Saccharomyces cerevisie.";
FEBS Lett. 239:179-184(1980).
-!-CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL 1,4-LINKED ALPHA-D-
GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REDUCING ENDS OF THE CHAINS
WITH RELEASE OF BETA--CHUCOSE.
-!-SIMILARITY: TO S. POMBE SPBC215.13.
                                                                                                                                    ---IINPMLSDETNICNG----KPVDGLTTL-----RNGTLVAFRGHYFWMLSPFSPPS 1005
                                                                                                                                                                 1559 TIDISNPKFDD----CVGHWAQEFIEKLTSLGYISGYPDGT-----FKPON 1600
                                            1454 YLRGYPDGSFRPERNITRAEAAVIF-----AKLL----GADESYGAQSASPYSD 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / AB972;
Salariell B.C., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                                                                                             -----TSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHM-
                                                                            ---VEMPE-----VTPDMDYLPRVPNQGI----
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                                                                                                                                                                                                                                                                                                                        POB640; POB068; Oreated)
01-8640; POB068; Mel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
01-GLUCOMMYLASE SI/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOMYLASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
STAI OR STAZ OR MAL5 OR YIRO19c.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
                                                                                                                                                                                                  PARRITEVWGIPSPIDTVFTRCNCEGKTFFFKD--SQYWRFTNDIKD 1050
                                                                                                                                                                                                                       1601 YIKRSESV----ALINRALERGPLNGAPKLEPDVNESYWAF-GDIMD 1642
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Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-89031230; PubMed-3141213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 TKKKTITSK-TCT---KKTTTPVPTPS-SSTTESSSAPV-----PTPSSSTTESSSAPV
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                                                                                                        Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
W; 91C00E2DBD61AA9D CRC64;
                                                                                                                                                                                                                                                                                                                                        Mismatches 483; Indels 171;
                                                                                                                                                                                                                                                                                                  DB 1; Length 1367;
                                                                                                                                                                 GLUCOAMYLASE S1/S2.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                  12.0%; Score 789.5; DB 1.
Llarity 28.4%; Pred. No. 7.9e-26;
Conservative 104; Mismatches 483.
                                                                                                                                                                                                                                                 136110
EMBL; M16165; AAA35015.1;
EMBL; X13857; CAA32069.1;
PIR; B26877; B26877.
PIR; A26877; A26877.
                                                                                                                                    Multigene family.
                                                                                                                                                                       1367
1367
817
874
                                                                          PIR; S48478; S48478.
SGD; S0001458; MUC1.
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Matches 301;
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Wreschener D.H.,

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P15941: P15942; P13931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;
O1-JAN-1990 (Rel. 13, Created)
O1-JAR-1990 (Rel. 14, Last sequence update)
O20-AUG-2001 (Rel. 40, Last annotation update)
MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEM)
(EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN)
(TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (FARACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN)
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Lancaster C.A., Peat N., Duhig T., Wilson D.,
Taylor-Papadimitriou J., Gendler S.J.;
"Structure and expression of the human polymorphic epithelial mucin gene: an expressed VNTR unit.";
                                                                                                                                                       -SVTIVINFTPTT-ITTIVCSTGT------NSAGETTSGCSPKTVTTTVPCST
                                                         ---TKAPKKPTSTKKPKTMPRVRKPKTTPTPR
                                                                                   1022 ---SESTITSPITPVTTVVSTIVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTIAPTP-
                                                                                                                                                                                        FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML
                                                                                                                    879 KMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Pancreas;
MEDLINE-90368716; PubMed-2394722;
Lan M.S., Batra S.K., Q1 W.N., Metzgar R.S., Hollingsworth M.A.;
"Cloning and sequencing of a human pancreatic tumor mucin cDNA.";
J. Biol. Chem. 265:15294-15299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligtenberg M.J.L., Vos H.L., Gennissen A.M.C., Hilkens J.; "Epistalin, a carcinoma-associated mucin, is generated by a polymorphic gene encoding splice variants with alternative amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Dubig Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D.; Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.";
                                                                                                                                                                                                                                                             SPFSPPSPARRITEVWGIPSPIDTVFTRC----NCEGKT 1033
                                                                                                                                                                                                                                                                                       1176 APSAPVTPATN-----AVPTTITT--TECSAATNAAGET 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biophys. Res. Commun. 173:1019-1029(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 265:15286-15293(1990).
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J. Biol. Chem. 265:5573-5578(1990).
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MEDLINE-90368715; PubMed-1697589;
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TISSUE-Breast carcinoma;
MEDLINE-90276413; PubMed-2351132;
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MEDLINE-91097524; I
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"Human epithelial tumor antigen cDNA sequences. Differential splicing may generate multiple protein forms.";
Eur. J. Blochem. 189:463-473(1990).
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PTM: HIGHLY GLYCOSYLATED (N-AND O-LINKED CARBOHYDRATES AND SIALIC,
                                                                                                                                                     MEDLINE-90276414; PubMed-2112460; Hareuveni M., Tsarfaty I., Zaretsky J., Kotkes P., Horev J., Hareuveni M., Tsarfaty I., Zaretsky J., Keydar I., Wreschner D.H.; Zrihan S., Welss M., Green S., Lathe R., Keydar I., Wreschner D.H.; A transcribed gene, containing a variable number of tandam repeats, codes for a human epithelial tumor antigen. cDNA cloning, expression of the transfected gene and over-expression in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  highly immunogenic region of a human polymorphic epithelial mucin pressed by carcinomas is made up of tandem repeats."; Biol. Chem. 263:12820-12823(1988).
                                                                                                                                                                                                                                                                                                                                                    Tsarfaty I., Hareuveni M., Horev J., Zaretsky J., Weiss M., Jeltsch J.M., Garnier J.M., Lathe R., Keydar I., Wreschner D.H.; Isolation and characterization of an expressed hypervariable gene coding for a breat-cancer-associated antigen."; Gene 93:313-318(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SECRETED FORM
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POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC. IT
     Smorodinsky N.,
Lathe R., Dion A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weiss M., Baruch A., Keydar I., Wreschner D.H.,
Preoperative diagnosis of thyroid papillary carcinoma by retranscriptase polymerase chain reaction of the MUCI gene.";
Int. J. Cancer 66:55-59(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buluwela L., Liu Q., Lugman1 Y.A., Gomm J.J., Coombes R.C., Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE FROM N.A.
MEDLINE-88330762; Pubmed-3417635;
Gendler S.J., Taylor-Papadimitriou J., Duhig T., Rothbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: VARIOUS VARIANTS ARE PRODUCED BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abb M., Siddiqui J., Kufe D.; Sequence analysis of the 5' region of the human DF3 "Sequence analysis of the 5' region of the human DF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lochem. Biophys. Res. Commun. 165:644-649(1989)
 D.H., Hareuveni M., Tsarfaty I.,
Zaretsky J., Kotkes P., Weiss M.,
                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 189:475-486(1990)
                                                                                                                                                                                                                                                                                                                                       MEDLINE-91033045; PubMed-1688329;
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MEDLINE=96183746; PubMed=8608966;
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TISSUE-Breast carcinoma;
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                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Breast carcinoma;
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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VARIES FROM 21 TO 125 IN THE NORTHERN EUROPEAN POPULATION. THE MOST FREQUENT ALLELES CONTAINS 41 AND 85 REPEATS.
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Pfam; PF01390; SEA; 1.
SMART; SM00200; SEA; 1.
PROSITE; P550024; SEA; 1.
Glycoprotein; Signal; Cytoskeleton; Actin-binding; Transmembrane; Repeat; Alternative splicing.
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MISSING (IN ISOFORM C).
MISSING (IN ISOFORM D).
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EXTRACELLULAR (POTENTIAL).
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CAA36477.1; ALT_SEQ.
AAB59612.1; ALT_SEQ.
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PIR: B35175; B35175.
PIR: S10218; S10218.
GlycoSuiteDB; P15941; -.
MIM; 158340; -.
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AAA35806.1;
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AAA35757.1;
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Query Match

Best Loca Matches

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                                        PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAPDNK 125
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                                                                                                                     ----KEPAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPK---E
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                                                                                        SAPITPKEPAPITIKSAPITPKEPAPITIKEP-----APITPKEPAPITIKEPAPITIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANDEM REPEATS OF Y-K-[PA]-K-[LP]-[ST]-Y-
            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLIC ADHESIVE PROTEIN) (FOOT
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: SECRETED.

TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.

PUM: THE DECAPEPTIDE A-K-P-S-Y-P-T-Y-K IS POST-TRANSLATIONALLY

MODIFIED AS FOLLOWING: THE SIXTH AND SEVENTH RESIDUES ARE

HYDROXYLATED AND THE PENULTIMATE IS A 3,4-DIHYDROXYPHENYLALANINE

(DOPA) DERIVED FROM TYROSINE.
                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=91025829; PubMed=1367451; Filpula D.R., Lee S.M., Link R.P., Strausberg S.L., Strausberg R.L.; "Structural and functional repetition in a marine mussel adhesive
                                                                                                                                                                                                                                                                                                                          "Evidence for a repeating 3,4-dihydroxyphenylalanine- and hydroxyproline-containing decapeptide in the adhesive protein of the mussel. Mvtilus edulis L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 TQHNKVSTSPKITTAKPINP------RP--SLPPNSDTSKETSLTVNKETTVET 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 KETITINKQISIDG--KEKIT---SAKETQSIEKTSAKDLAPISKVLAKPIPKAETITKG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 PIKTTYNAKTNYPPVYKPKMTYPPTYKPKPSYPPTYKSKPTYKPKITYPPTYKAKPSY-- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 PALTTPKEPTPTTPKE----PASTTPKEPTPTTIKSAPTTP-----KEPAPTTKSAPTT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSSEL, MYLLIUS edulis L.";
J. Biol. Chem. 258:2911-2915(1083).
I. FUNCTION: PROVIDES ADHESIVENES TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.
                                                                                                  Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 556.5; DB 1; Length 875; larity 28.7%; Pred. No. 1.7e-16; Conservative 106; Mismatches 375; Indels 195;
                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS. MEDLINE-83135732; Pubmed-6298211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-[ST].
6EA85312748CAACE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biotechnol. Prog. 6:171-177(1990)
                                                                                                                   Eukaryota; Metazoa; Mollusca; B. Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875 AA; 100412 MW;
                                                                       PROTEIN 1) (MEFP1) (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                  NCBI_TaxID=6550;
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                                                                                                                                                                                                                                                                                                               Waite J.H.;
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Best Local Si
Matches 272,
                                                                                                                                                                                                                                        protein.
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264
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                                                                                                                                                                                                                                                                                                409
                                                                                                                                                                                                                                                                                                                            420 ITTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPE 479
                                                                                                                                                                                                                                                                                                                                                                                                                      533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 PKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTT----PKE 589
                                                                                                                                                                                                                                                                                                                                                     551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPTTPKEPAPTTPKGT---APTTLKEPA--PTTPKKPA--PKELAPTTTKG-PTSTTSD 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              739
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                                                                                                         PKEPAPTTTKEPA--PTTPKEPA------PTTTKEPA-PTTTKSAPTTPK--EPAPTT
                                    P----PTYKAKPSYPPTYKAKPSYPPTYKAKPTYPSTYKAKPSYPPTYKAKPTY
                                                                             265 PKKPA--PITPKEPA--PITPKEPT--PITPKEP---APTIKEPAPTIPKEPA--PTAPK
                                                                                                                                                            KPA--PTTPKEPA--PTTPKEPA--PTTTKEPS--PTTPKEPA-PTTTKSAPTTKEPA-
                                                                                                                                                                                        458 KPT-----YPSTYKA----KPSYPASYKAKPSYPPTYKSKSSYPSSYKPKKTYPPTYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 EPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKE----PAPTTPKETAPTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 KPAPTTPKETAPTTPKEPA--PTTPKKPA-PTT----PETPPPTTSEVSTPTTKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 PATYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYKAKPTYPSTYKAKPSYPPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAKPSYP----PTYKAKPSYPPTYKAKPTYPSTYKAKPSYPPTYKPKISYPPTYKAKPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 AKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTQDTTPFKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              778 TYKSKSIYPSSYKPKKTYPPT---YKPKLTYPPTYK------PKPSYPPSYKPKITYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTIHKSPDESTPELSAEPTPKALENSPK----EPGVPTT--KTPA----ATKPEMTTT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-2379 FROM N.A.
MEDLINE-99018118; PubMed-9799793;
Glockner G., Scherer S., Schattevoy R., Boright A., Weber J.,
Tsul L.C., Rosenthal A.;
"Large-scale sequencing of two regions in human chromosome 7q22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 857 ISTKKPKTMPRVRKPKTTPTP------RKMTSTMPELNPTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STYKLKPSYPPTYKSKTSYPPTYNKKISYPSSYKAKTSYPPAYKPTNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZAN_HUMAN STANDARD; PRT; 2700 AA. 097439; 000218; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZONADHESIN (FRAGMENT)
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CONFLICT
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CARBOHYD
             CARBOHYD
CARBOHYD
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                                                                                                                                                                           -!- SUBDNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
-!- TISSUE SPECIFICITY: IN TESTIS: PRIMARLLY IN HAPLOID SPERMATIDS.
-!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
-!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OYLDUCTAL ISTHMUS.
-!- DOMAIN: THE WYED DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
                                                                                                              zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEATS (APPROXIMATE)
  analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
                                                                                            3ao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAM 1.
MAM 2 (PARTIAL).
MAM 4.
66 X HEPTAPEPTIDE REPI
(MUCIN LIKE DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARS, 0023/2;
InterPro; IPR000561; EGF-like.
InterPro; IPR000998; MAM.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002919; TILa.
InterPro; IPR003328; TILa.
InterPro; IPR001007; VWFC.
InterPro; IPR001007; VWFC.
InterPro; IPR001846; Vwd.
Pfam; PP00824; TILa; 4.
Pfam; PP008245; TILa; 4.
Pfam; PP00945; TILa; 4.
Pfam; PP00941; Vwd; 4.
PRINTS; PR001217; PRCHEXTENSN.
SMART; SM00137; MAM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWFD 4
                                                                     IISSUE=Testis;
MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Transmembrane; Cc

NON_TER 1 1 1

DOMAIN <1 109 Mi

DOMAIN 112 136 Mi

DOMAIN 161 326 Mi

DOMAIN 322 446 Mi

DOMAIN 483 951 66
                                                       SEQUENCE OF 2338-2700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF053356; AAC78790.1; -. EMBL; U83191; AAC51208.1; -.
                              Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00011; VWC_def; 3. SMART; SM00216; VWD: 3. PR005ITE; PS001186; BGF_2; 3. PR05ITE; PS00746; MAM_1: 1. PR0SITE; PS50060; MAM_2; 4.
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1861
2292
2684
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                     reveals 17
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DOMAIN
CARBOHYD
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480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPHPSPTA-TGLAALVMSPHAPSTPMTSV---ILGTTTTSRSSTGMSCP-PNARYESCAC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAKDLAPISKVLAKPIPKAETITKGPALITPKEPIPTIPKEPASTTPKEPT-----PTII 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EKPSIPTEK---PTISMEETIISTEKPTICPEKPTIPTEK---PTIPTEKSTISPEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKSAPTTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 PIPTIPEEPAPTIPKAAAPNIPKEPAPTIPKEPAPTIPKEPAPTIPKETAPTIPKGTAPT
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01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-1992 (Rel. 12, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2700;
                                                                                                                                                                                                                                                                                     NNOKMA -> RAGPGP (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                             80E60CC0B12277B1 CRC64;
                                                                                            (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                     (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       8.5%; Score 555.5; DB 1;
32.6%; Pred. No. 4.9e-16;
iive 64; Mismatches 240;
                                                                                                                                                                                                                      (GLCNAC.
                                                                  (GLCNAC.
                                    (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                       M.W.
                                                                                                                                                                                                                                                                                                                                                 AA; 293013
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 32.6
Matches 199; Conservative
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         403
1023
1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                   PENTAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AETTIK-GPALTIP--KEPIPIT-----PKEPASITPKE---PIPITIKSAPITPKEPAP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 TTTKSAPTTPKEP-----APTTTKEPAPT---TPKEPAPTTTKEPAPTTTKSAPTTPKE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 PSPQV--QPPPT--YSPPPPTHVQPTPSPPSRGHQPQPPTHRHAPPTHRAPPTHQPSPL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---APTIPKEPSPITIKEPAPTIPKEPAPTIPKKPAPTIPKEPAPI----IPKEPAPTITK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHLPPSPRRQPOPTYSPPPAYAQSPQPSPTYSPPPTYSPPPSPIYSPPPAYSPSP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 PPTPTPTFSPPPPAXSPPPTYSPPPTYLPLPSSPIYSPPPVXSPPPPPSXSPPPTYL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 APTTPEEPTPTTPEEPAPTTPKAAAP---NTPKEPAPTTPKEPAPTTPKEPAPTTPKETA 530
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                              24 AEATTOYGGYLPPPVTSQPPPSSIGLSPPSAPTTTPPSRGHVPSP---RHAPPRHAYPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHGHLPPSVGGPPPHRGHLPPSRGFNPPSPVISPSHPPPSYGAPPPSHGPGHLPSHGQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPK----EPAPTTTKSAPTTTKEPAPTTTKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 KPAPT---APKEPAPTTPKETAPTTPKKL-TPTT-----PEKLAPTTPEKPAPTTPEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                            SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PERSER(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAINS THE SER-PRO(4) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S06733; S06733,
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X APPROXIMATE TANDEM REPEATS. 641DD2278AB28524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 551; DB 1; Length 620
27.2%; Pred. No. 2.1e-16;
IVe 64; Mismatches 304; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65406 MW;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13885; CAA32090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.28;
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73
151
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236
205
499
620 AA;
                                                                     SEQUENCE FROM N.A.
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Best Local Similarity
Matches 170; Conserv
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SEQUENCE
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DOMAIN
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539 PPPRQIHSPPPPHWQPRIPTYGQPPSPPTFSAPPPRQIHSPPPHRQPRPPTYGQP 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (MAR-1994) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHITCH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEH IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILEMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF AXONAL CALIBER.
PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89089138; PubMed-3145094; Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.; "The structure of the largest murine neurofilament protein (NF-H) as revealed by cDNA and genomic sequences."; Eaven Res. 464:217-231(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534
TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
                                                    PTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEP
                                                                                         P-----LPPTYSPPPPAYSPPPPTYSPPPTYSPPPPAYAQPPPPTYSPPPAYSP
                                                                                                                          591 APTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKE
                                                                                                                                                             PPPSPIXSPPPPQVQPLPPTFSPPPRRIHLPPPPHRQP----RPPTPTYGQPPSPPTFSP
                                                                                                                                                                                                  TAPTTPKEPAPT - - TPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Julien J.-P., Cote F., Beaudet L., Sidky M., Flavell D., Grosveld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mushynski W.; "Sequence and structure of the mouse gene coding for the largest neurofilament subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                  NFH_MOUSE STANDARD; PRT; 1087 AA.
P19246; Q61959;
O1-NOV-1990 (Rel. 16, Created)
O1-AGG-1992 (Rel. 23, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
                                                                                                                                                                                                                                                                         PTPKALENSPKEPGVPTTKTPAATKP 734
                                                                                                                                                                                                                                                                                                                  612
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STRAIN-SWISS WEBSTER; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-3220257;
                                                                                                                                                                                                                                                                                                   | : | : | | | PSP-----PTTYSPSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP-APTITKEPAPTIPKEPAPTITKEP----APTITKSAPTIPKEPA----PTIPKKPA- 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 VIVEGQTEEIRVTEGYTEEEDKEAQGQEGEEAEEGEEKEEEELAAATSPPAEEAASPEKE 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 EECRIGFGPSPFSLTEGLPKIPSIST--HIKVKSEEMIKVVE------KSEKET 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAGSGLDNGDFKVT----TPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKET 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                             SLU-RICH (ACIDIC).
50 x 6 AA TANDEM REPEATS OF K-S-P-A-E-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Mismatches 330; Indels 158;
                                                                                                                                                                                                     Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1087;
                                                                                                                                                                                                                                                                                                                                                                     K -> QA (IN REF. 2 AND 3).
A -> AR (IN REF. 2 AND 3).
C -> T (IN REF. 2 AND 3).
L -> G (IN REF. 2 AND 3).
P -> PREAKES (IN REF. 3).
MISSING (IN REF. 3).
G -> A (IN REF. 3).
T -> N (IN REF. 2 AND 3).
WW, 57BAC76A38EDICB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 533; DB 1;
Pred. No. 1.9e-15;
                                                                                                                                                                                                                                                                        50 x 6 AA TAI
GLU/LYS-RICH
                                                                                                                                                                                                                                                                                                                            LINKER 12.
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COIL 1B.
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LINKER 2.
                                                                    COIL 2B.
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ilarity 27.5%;
Conservative 8
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                                                                                                                                                                       mac, interpro; IPR001664; IF. Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                               261
283
283
287
408
1133
1199
281
712
712
814
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les 216; Conserva
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814
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DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN EPIMASTIGOTES AND NO DETECTABLE IN AMASTIGOTES.
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                                                                                                                                                                                                                                                                                                                                           1035 ---PK-MEAKVKEDDKSLSKEP--SKPKTEKAEKSSSTDQKESQPPE-----KTTEDKA 1082
                                                                                                                                                                                                                                           1006
                                                                                                                                                                                                                                                                                       767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             849 RP--PEQVKSPAKEKAKSPE--KEEAKTSEKVAPKKEEVKSPVKEEVKAKEPPKKVEEEK 904
                                                                                                                                                           530 APTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD--KPAPTTPKGTAPTTP 587
                                                                                                                                                                                                                 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN)
367 TKSAPTTPKE-PSPTTTKEPA----PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION.
MEDLINE-91376547; PubMed-1896773;
Prioli R.P., Mejia J.S., Aji T., Aikawa M., Pereira M.E.A.;
"Trypanosoma cruzi: localization of neuraminidase on the surface of
                                                                                                                                                                                                                 588 KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTT
                                                                                                                                                                                                                                                                      648 PKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSA
                                                                                                                                                                                                                                                                                                                           EPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETA
                                                                                                                                                                           SPAAVKSPGEAKSPGEAKSPAEAKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEK
SPAAVKSPGEAKSPGEAKSPAEAKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEK
                                                                      TPTTPEE-PAPTTPKAAAPNTPKEPAPTT----PKEPAPTTP----KEPAPTTPKET
                                                     TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pereira M.E.A., Mejia J.S., Ortega-Barria E., Matzilevich D.,
                                                                                                                                                                                                                                   1162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SILVIO X-10/4;
MEDLINE=91277609; PubMed=1711561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma cruzi.
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                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISCELLANEOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE INCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 PTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA----PT
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100; Mismatches 212; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 530.5; DB 1; Length 1162;
                                   SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES. SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                              PIR; JH0557; JH0557.
HSSP, P29768; DIL.
InterPro; IRP002866; BNR.
Pfam; PF02012; BNR; 2.
Hydrolase; Glycosidase; Glycoprotein; Repeat; GPI-anchor;
                                                                                                                                                                                                                                                                      BNR 1.
BNR 2.
BNR 3.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CANTON-S;
RA BALLINE-93165730; PubMed-8434015;
RA BALLINE-93165730; PubMed-8434015;
RA BALLINE-97365730; PubMed-8434015;
RA DICOSOPHILA Photoreceptor cell-specific protein, calphotin, binds
RT A Drosophila photoreceptor cell-specific protein, calphotin, binds
RT Calcium and contains a leucine zipper.";
RD Froc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
C-I- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOL.
C-I- SUBURIT: HOMODINER (PROBABLE).
C-I- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.
C-I- SUBCELLULAR LOCATION: CYTOPLASMIC; CC COMPONIND EXES AND OCELLI.
C-I- COMPOUND EXES AND OCELLI.
                 Martin J.H., Benzer S., Rudnicka M., Miller C.A., "Calphotin: a Drosophila photoreceptor cell calcium-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
PITSEVSTPITIKEPITIHKSPDESTP-ELSAEPTPKALENSPKEPGVPITKTPAATKPE 735
                                                                                                                                                                                                                                                                          CPN OR CAP.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Biphydroidea; Drosophilidae; Drosophila.
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I -> T (IN REF. 2).
T -> A (IN REF. 2).
P -> PP (IN REF. 2).
VQ -> AP (IN REF. 2).
I -> V (IN REF. 2).
S -> T (IN REF. 2).
A -> E (IN REF. 2).
C -> T (IN REF. 2).
C -> E (IN REF. 2).
C -> E (IN REF. 2).
C -> E (IN REF. 2).
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01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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MEDLINE=93165729; PubMed=8094559;
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EMBL; L05080; AAA28420.1; --
PIR; A47282; A47282.

FlyBase; FBgn0010218; Cpn.
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CONFLICT 36
CONFLICT 43
CONFLICT 76
CONFLICT 100
CONFLICT 126
CONFLICT 126
CONFLICT 154
CONFLICT 534
CONFLICT 699
CONFLICT 699
CONFLICT 703
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CONFLICT 703
CONFLICT 703
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                                                              736 MT 737
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Q02910;
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CPN_DROME
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                                                                                                                                                                                                                                                            177 AAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPECVAPLIPEVSVVATK 236
                                                                                                                                                                                                                                                                                                                                                    297 ETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETPEVASVAVAETTPPVVPPV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                    TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKE------PAPTTPKKPAPKE 557
                                                                                                                                                             62 VTIPAPAPIAAASVTPVASVAPPVVAAPTP----PAASPVSTPVAVAQIPVAVSAPVAP 116
                                                                                                                                                                                                                                                                                      41.1
                                                                                      147 APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT 202
                                                                                                                                      203 PKEPAPITIKSAPITP-KEPAPITIKEPAPITPKEPAPITIKEPAPI----TIKSAPITP 257
                                                                                                             8 SPVSAPVAAPVTPSAVAAPVQVVSPAAVAP-----APAAPIAVTPVAPPPTLASVQPAT 61
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 TLKEPA-----PITPKKPAPKELAPTIT----KGPTSTISDKPAPTT----PKETAPTI
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                                                                                                                                                                                                                                                                                                       412 TTP-----KEPAPITIKKPAPIAPKEP---APTIPKEI-----APTIPKKLIPI
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                                                                                                                                                                                                                                       ---TTTKSA
                                       8.1%; Score 53v, -- 26.2%; Pred. No. 2e-15; +ive 73; Mismatches 433; Indels 152; +ive 73; Mismatches 433; Indels 152;
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                                                                                                                                                                                                                                       PKEPA--PTAPKKPAPTTPKEPAPTTPKEPAPTTTKE-PSPTTPKEPAP--
     2110417E0B0E7CFE CRC64;
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       84781 MW;
                                                                    233; Conservative
          AA;
                                             Query Match
Best Local Similarity
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Q25434;
          SEQUENCE
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FP1_MYTCO
ID FP1_MY
AC Q25434
DT 30-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADHESIVE PLAQUE MATRIX PROTEIN.
NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-{IP}-[ST]-Y-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 APTITKEPAPTITKSAPTIPKEPAPIT--PKKPAPTIPKEPAPTI----PKEPIPIT--P 289
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                                                                                                                                                                                                                                                                                                                                                                                                                    "Adhesive protein cDNA sequence of the mussel Mytilus coruscus and "Adhesive protein cDNA sequence of the mussel Mytilus coruscus and lits evolutionary implications.";
J. Mol. Evol. 43:348-356(1996).
J. Mol. Evol. 43:348-356(1996).
J. Mol. Evol. 63:48-356(1996).
J. Mol. Evol. 63:48-356(1996).
J. Mol. Evol. 74E STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S PRODUCE ONE OF THRRADS, CALLED A BYSSUS, FORMED BY A PHERIVOR COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.
J. SUBCELLULAR LOCATION: SECRETED.
J. TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
J. TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
J. DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPRATS OF A DECAPPETIDE.
J. PPW: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND ALSO TYROSINE (THUS PRODUCING DOPA = 3,4-DIHYDROXYPHENYLALANINE).
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MCFP1).
                                                                                                                           Mytilus coruscus (Sea mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=42192;
                                                                                                                                                                                                                                                                                                                                                                       E., Yamazaki F., Odo
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NONAPEPTIDE
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InterPro; IPR002964; Adhesive_plaq.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                          MEDLINE=96394686; PubMed=8798340;
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PRINTS; PR01217; PRICHEXTENSN.
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Best Local Similarity
Matches 282; Conserv
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-PTYKRKPSYT----PYKPKTTYPPTYKPKISYPSIYKPKASYVSSYKSKKTYPPTYKP
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MEDLINE-93077556; PubMed-1447205;
MEDLINE-93077556; PubMed-1447205;
MEDLINE-93077556; PubMed-1447205;
MEDLINE-93077556; PubMed-1447205;
P-domains as shuffled cysteine-rich modules in integumentary mucin C-1 (FIM-C-1) from Xenopus laevis. Polydispersity and genetic polymorphism.";
Dolymorphism.";
J. Blol. Chem. 267:24620-24624(1992).
                           KEPAPTIKEPAPTIPKEPAPT-APKKPAPTIPKEPAPTIPKEPAPTITKEPSPITPKEPA
                                                                                                             PTPYKOKPSYPPIYKSKSSYPTSYKSKKTYPPTYKPKITYPPTYKPKPSYPPSYKPKKTY
                                             APT-TPK-----EPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAP----TTPKK
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                                                                                  PTTTKSAPT----TTKEPAPTTTKSAPTTPKEPSPTTTKEPA-PTTPKEPAPTTPKKP-
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
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NCBI_TaxID=8355;
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SEQUENCE FROM N.A.
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FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMENT. SUBCELLUAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: A NUMBER OF DIFFERENT FORMS OF THE PROTEIN MAY BE PRODUCED BY ALTERNATIVE SPLICING.
FISSUE SPECIFICITY: SKIN.
PIM: EXTENSIVELY O-GLYCOSYLATED.
SIMILARITY: CONTAINS 6 P-TYPE (TREVOL) DOMAINS.
                                                                                                                                                                                                                                                                                                         APPROXIMATE TANDEM REPEATS, THR-RICH.
                                                                                                                                                                                                                  APPROXIMATE TANDEM REPEATS,
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P-TYPE 3.
12 X APPROXIMATE TANDEM REPEATS,
                                                                                                                                             HSSP; P04002; IWFA.
InterPro; IMFA.
InterPro; IRR00519; P_trefoil.
Pfam; PF00088; Lrefoil; 6.
SMART; SM00018; P; 6.
PROSITE; PS00025; P_TREFOIL; 6.
Repeat; Amphibian skin; Glycoprotein; Alternative splicing.
NON_TER 81 144
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P-TYPE 4.
P-TYPE 5.
P-TYPE 5.
P-TYPE 6.
BY SIMILARITY.
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                                                                                                                                                                                                                                        176 TPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTFK 235
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                                                                                                                                                                                                                                                                                                                       --PITKEPAPI---TPKEPAPIAPKKPAPITPK------EPAPITPKEPAPITKE 338
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                                                                                                                                                                                                TTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEP 175
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                                                                                                                                                           Score 509.5; DB 1; Length 662;
                                                                                                                             F085277F1ED2FD40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00623; RNA_pol_A; 1.

Pfam; PF01854; RNA_pol_A2; 1.

PROSITE; PS00115; RNA_POL_II_REPEAT; 43.

Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Repeat; DNA-binding; Nuclear protein; Phosphorylation; Zinc-finger.
ZN FING 7 7 87 C2H2-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  RNA(N).

-1 SUBDATT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.

-1 SUBDATT:

-1 SUBCELLULAR LOCATION: NUCLEAR.

-1 PIT SHORDEN TO RESIDIES REPEATS CAN BE HIGHLY PHOSPHORYLATED.

-1 PITE PHOSPHORYLATION ACTIVATES POLZ.

-1 PHE PHOSPHORYLATION ACTIVATES POLZ.

-1 MISCELLANDOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOK, POLYMERASE II FOR THE MRNA PRECURSOK, AND PARABES II FOR THE MRNA PRECURSOK, AND TRNA GENES.

-1 SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=92178992; PubMed=1542581;
Mintzerith M., Acker J., Vicalire S., Vigneron M., Kedinger C.;
Wintzerith M., Acker J., Vicalire S., Vignerase II largest subunit.";
"Complete sequence of the human RNA polymerase II largest subunit.";
Nucleic Acids Res. 20:910-910(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1).
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                                                                                                                                                                Euteleostomi;
                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                             1970 AA
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EMBL; X74874; CAA52862.1; --
EMBL; X74873; CAA52862.1; JOINED.
EMBL; X74872; CAA52862.1; JOINED.
EMBL; X74871; CAA52862.1; JOINED.
EMBL; X74870; CAA52862.1; JOINED.
EMBL; X74870; CAA52862.1; JOINED.
EMBL; X74870; CAA52862.1; JOINED.
INF, S21054; S21054.
InterPro; IPR000684; ENA_POILI_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000722; RNA_pol_A. IPR002879; RNA_pol_A2.
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1067
1449
                                  STANDARD;
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                                    RPB1_HUMAN
P24928;
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MEDLINE-87280135; PubMed-3038894;
MEDLINE-87280135; PubMed-3038894;
"Cloning and sequence analysis of the mouse genomic locus encoding the largest subunit of RNA polymerase II.";
Blol. Chem. 262:10695-10705(1987).
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01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1).
POLR2A OR RPO2-1 OR RPII215.
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MEDLINE-86068017; PubMed-2999785;
Corden J.L., Cadena D.L., Ahearn J.M. Jr., Dahmus M.E.;
"A unique structure at the carboxyl terminus of the largest subunit
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Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                      95;
                                                                                                                                        Length 1970;
                                                                                                                                                                                                              Indels
            6876FC25692A657E CRC64;
                                                                                                       Ouery Match 7.7%; Score 503.5; DB 1; Best Local Similarity 33.3%; Pred. No. 5e-14; Matches 181; Conservative 101; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1970 AA.
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    1970 AA;
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P08775:
    SEQUENCE
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RPB1_MOUSE
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                                                                                                                                                                                                   POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION. NUCLEAR.
-1- PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
-1- PTM: THE PHOSPHORYLATION ACTIVATES POL2.
-1- MISCELLANBOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYCTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MINA PRECURSOR, AND POLYMERASE III FOR SAND TRNA GENES.
-1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wintzerith M., Acker J., Vicaire S., Vigneron M., Redinger C.; "Complete sequence of the human RNA polymerase II largest subunit."; Nucleic Acids Res. 20:910-910(1992).
-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTIC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIPITPKEPASTIPKE-PIPITIKSAPITPKEPAPITIKSAPITTPKE-----PAPITIKE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - SPTSPSYSPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-1725
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                                                                                                                                                                                                                                                                                     -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                              RNA(N).
-1- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP--APTTPKEPTP
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of eukaryotic RNA polymerase II.";
Proc. Natl. Acad. Sci. U.S.A. 82:7934-7938(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 498.5; DB 1;
llarity 33.1%; Pred. No. 7.9e-14;
Conservative 101; Mismatches 168;
                                                                      REVISIONS, AND PRESENCE OF AN ADDITIONAL EXON MEDLINE=92178992; Pubmed=1542581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFECT. A28420.
MGD; A28430.
MGD; MGI:98086; Rpo2-1.
InterPro; IPR000684; RNA_polII_repeat.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M12130; AAA40071.1; -
EMBL; M14101; AAA40071.1; JOINED.
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.
                                                                                                                                                                                                     PAPTTPKETAPTTPKEP--APTTPKKPAPTTPETPPPTTSEVSTPTTKEPTTIHKSPDE 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEFH OR NFH.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                  525 TPKETAPTTPKGTAPTTLKEPAPTTPK-KPAPKELAPTTTKEPTSTTSDKPAPTTPKGTA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breen K.C., Robinson P.A., Wion D., Anderton B.H.; Partial sequence of the rat heavy neurofilament polypeptide (NF-H). Identification of putative phosphorylation sites."; FEBS Lett. 241:213-218(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolles \hat{P}_{\cdot,\cdot} , "The large neurofilament subunit (NF-H) of the rat: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89184647; PubMed-2928342;
MEDLINE-89184647; PubMed-2928342;
Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D.,
Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubin L.;
"Cloning of a cDNA encoding the rart high molecular weight enurofilament peptide (NF-H): developmental and tissue expression
the rat, and mapping of its human homologue to chromosomes 1 and
22.";
                                                                                                                                    584 PITPKEPAPTIPKEPAPTIPKGTAPTILKEPAPTIPKKPAPKELAPTITKGPT-STISDK
                                                                                      SP-SYSPTSPKYT------PTSPSYSPSYSPEXTPASPK--XSPTSPKXSPTSPK-YS
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SEQUENCE OF 37-831 FROM N.A.
SEQUENCE OF 37-831 FROM N.A.
MEDLINE=88309090; PubMed=245/365;
Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L., Jolles P.;
PTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEP -- APT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robinson P.A., Wion D., Anderton B.H.; "Isolation of a cDNA for the rat heavy neurofilament polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                  NFH_RAT STANDARD; PRT; 831 AA.
P16884, 066386;
01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in situ detection.";
Biochem. Biophys. Res. Commun. 154:1099-1106(1988)
                                                                                                                                                                                                                                                                                                                                                                                              831 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=89065087; PubMed=3143606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PITPKEPA----PITPKEP----TPITPKEPAPITKEP----APITPKEPA----PIA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDTSTIQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTINKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 KEAQGEEEEEBEEGGEEAATTS-----PPAEEAASP----EKETKSPVKEEAKSPAEAKS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAEAKSPAEAKSPAEVKSPAVAKSPAEVKSPAEAKS-PAEAKSPAEVKSPATVK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGEAKSPAEAKSPAEVKSPABAKSPAEAKSPASVKS-PGEAKSPAEAKSPAEVKSPATV 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEP---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEATS OF K-S-P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 497; DB 1; Length 831; 27.6%; Pred. No. 4.3e-14; ive 59; Mismatches 307; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 X 3 AA TANDEM REPEATS OF K-
L-> I (IN REF. 2).
L-> T (IN REF. 2).
M-> T (IN REF. 2).
K-> W (IN REF. 1).
A-> V (IN REF. 1).
A-> V (IN REF. 1).
P-> E (IN REF. 2).
RX-> K (IN REF. 2).
RX-> K (IN REF. 2).
RX-> K (IN REF. 2 AND 4).
P-> S (IN REF. 2 AND 4).
A-> V (IN REF. 2 AND 4).
                                                                                                                                                                                                                                                                                    EMBL; M37227; AAA41693.1; ALT_FRAME.
EMBL; X13804; CAA32038.1; ALT_FRAME.
EMBL; M21964; AAA41695.1; -
EMBL; J04517; AAA41692.1; -
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Pfam; PF00038; filament; 1.
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PIR; A25649; A25649.
PIR; B25649; B25649.
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Matches 195; Conserv
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	PKKPAPTTPKEPAPTTPKI	AKSPAEAKSPAGAKPP	APTTTKSAPTTPK	 VKEGAKSLA			APTTPEEPTPTTPEEPAPT	:	PKGTAPTTLKEPAPTTPKK	KKEEAKEKKAAAPEE	TPKEPAPTTPKGTAPTTLK	:          SEKEK	ТТРКЕРАРТТРККРАРТТР	::       AKEEDKGLPQEP
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Sequence 103, Appl
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Sequence 75, Appl
Sequence 103, Appl
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1 MAWKILPIYLLILLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1229
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/laa/fa_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-083-116-5

US-09-083-116-2

US-08-479-537A-2

US-08-179-537A-5

US-08-179-535-132

US-08-177-559B-103

US-08-177-578B-103

US-08-177-578B-103

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                                                                                                                                                                                                                                                                                                                                           212252 seqs, 22503292 residues
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Listing first 45 summaries
                                                                          OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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					RESULT 1 US-09-103-429A-4	RESULT US-09-10
	ALIGNMENTS					
	PCT-US94-04496-28	S.	1187	9.0	367.5	<b>4</b>
28	US-08-545-860D-28	m	1187	9 1	367.5	4.
28,	US-08-320-559-28	-	1187	9.	367.5	4.
31.	US-08-397-633A-31	-	762	9.6	368	4.2
120	US-08-642-255-120	7	762	5.6	368	41
62,	US-08-642-255-62	П	1064	2.6	370.5	40
26	US-08-397-633A-26	-	762	5.6	371	36
117	US-08-642-255-114	~	762	5.6	371	38
Sequence 84 Appl	US-08-707-237A-84		761	5.6	371	37
4	US-08-904-263A-4	m	1231	5.7	373.5	36
2	US-08-325-267A-2		1537	5.7	374.5	3.5
ي ا	US-09-219-849-6	4	960	5.7	376	34
9	PCT-US95-10661A-6	S	1848	5.8	381	33
2	US-08-296-791-6	4	1848	5.8	381	32
36.	US-08-397-633A-36	-	682	6.1	398.5	31
126	US-08-642-255-126	Н	682	6.1	398.5	30
65,	US-08-478-029A-65	4	408	6.2	404.5	50
Segmence 65, Appl	US-08-475-411A-65	4	408	6.2	404.5	28

S PEC V MAN PE P P P P P P P P P P P P P P P P P P	SUTURER: Petentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NATA: APPLICATION NATA: CLASSIFICATION: 800 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390 REFERENCE/DCOKET NUMBER: BTI-39 TELEPHONE: (607) 256-200 TELEPHONE: (607) 256-200 TELEPHONE: (607) 256-328 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: amino acid acids TYPE: amino acid acids TYPE: amino acid STRANDEDNESS: single MOLECULE TYPE: protein HYPOTHETICA: NO ANTI-SENSE: NO ORIGINAL SOURCE: CREATION TICHOPLUSIA ni NSANT-SENSE: NO STISSUE TYPE: peritrophic membrane
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Score 522; DB 4; Length 805; Pred. No. 1.9e-27;

7.98;

Query Match Best Local Similarity

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Query Match
Best Local Similarity
Matches 295; Conserv
Palo Alto
                     USA
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                       149 TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAP-----TTP 203
  Gaps
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                                              9 TALGLVAARPEVSDAEKNPALHEPHPDXP--PAEQXXLLPXEYDCTKFYYCEYGLKFIAP
                                                                         ---TKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTK
                                                                                                                                             120 QAPTITTQATTIT-----QAPTITQAPTIT----QATTIQAPTIT----
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   211;
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     Mismatches
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     33;
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TITLE OF INVENTION: PEPT
TITLE OF INVENTION: FOR
TITLE OF INVENTION: FOR
TITLE OF INVENTION: SPEC
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
      Conservative
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STREET: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 KVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTT
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                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7%; Score 508; DB 3;
21.3%; Pred. No. 4.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                        NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTTPKEPAPTTTKKPAP----------
                                                                                                                      MBER: US/08/928,361B
12-SEP-1997
                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - PTPTT-
                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 100;
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-24-
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FUNCTH: 1837 amino acids
ZIP: 94300-1030
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.3%;
                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-928-361B-5
                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 12-SEP
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366

426

726 410

315 999

486

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135 TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 190
                                                                                                                                                                                                                                                                                                                                         TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTT----PKEPTPTTPKEPAPTTKEP--- 299
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                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                            -----YPPTYK--AKPS------YPPTYKPKTYPPTYKPKLTYPPTYKPKP 92
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                                                                                                                                                              Indels 175;
                                                                                                                                      Length 744;
                                                                                                                             Query Match
7.7%; Score 506.5; DB 6;
Best Local Similarity 29.9%; Pred. No. 1.9e-26;
Matches 239; Conservative 78; Mismatches 308;
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 KETATITEKITESKITATIT 783
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720 YKAKPTYPSTYKAKPTYPST 739
                                                                             LENGTH: 744
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US-09-103-429A-3
                                                              ; SEQ ID NO:25;
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254 РТТРКБРАРТТРККРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТАРК 313
                                                                                                                                                                                                                                                                                                                                              ---APATTPEDDDIDP--PLPNDPINP 699
                                                                                                                                                                                                                                                                                                                    641 DKPAPTTPKETAPTTPKEPAPTTPKKP 667
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08700651B Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
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US-08-700-651-5
        386 APTT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 PGPPAE-TTQAPATT----QAPTTTQAPTTTT------QAPTTTTQ--ATTTTQAP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 TTPKEPAPTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 PIPKAETITKGPALTIPKEPTPTTPKEPASTTPKEPTPTIKSAPTTPKEPAPTTKSAP 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 DGEISPAPPVTEGNEDEDIDIGDLLDNGCPANFEIDWLLPHGNRCDKYYQCVHGNLVERR
                                         APPLICANT: Granados, Robert R
APPLICANT: Granados, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PTTTKEPSPTTPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 786;
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 498.5; DB 4; ilarity 29.1%; Pred. No. 7.1e-26; Conservative 25; Mismatches 207;
                                                                                                                                      1118 No. 6187558th Tioga
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390
REPERNCE/DOCKET NUMBER: 31-39
TELECOMMUNICATION INFORMATION:
TELEPRAN: (607) 256-2000
TELEPRAN: (607) 256-3608
INFOREMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Trichoplusia ni
TISSUE TYPE: peritrophic membrane
Sequence 3, Application US/09103429A Patent No. 6187558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 786 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
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les 200; Conservé
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                                                                                                                                                                                                            USA
                                                                                                                                                                              Ithaca
                                                                                                                                                                                                                          14850
                                                                                                                                               ADDRESSEE:
STREET: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-429A-3
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 200;
                                                                                                                                                                                             STATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DETERN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: USCON, RICHARD, C.
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIGIUM PARVUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.194 4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15 41; ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 193 240 : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : ----TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 133 29 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDJSTTQHNKVSTSPKÍÍTAKPINPRPS 88 463 EKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNT--PKEPAPTTPKEPAPTTPKE 520 633 TAAPIT-AAPAPUTUTUPPTAAPITAAPITVAH------APNITAAPUTITS 677 194 TIIKSAPTTPKEPAPTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSA 159 APCNSENSFEQGQIEDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTT-----521 PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPK APTAAPTAAPTTAVPEIPTTVTSPPTAAPTTAAP---ANTT-----VTVPP GTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS 421 ADFSIDHLLPHESDCGQYLQCVHGQTIARPCPGNLHFSPATQSCESPVTAGCQVFECDSD ---PKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTP 481 NQCISTAAPTAAPTAAPTAAPTAAPTA-APSTVVPPATPPATAAPVPPTT---AIPT--Indels 442; Length 1721; -APTTPKKPAPTT Query Match
7.4%; Score 489; DB 3; L.
Best Local Similarity 22.1%; Pred. No. 7.8e-25;
Matches 284; Conservative 82; Mismatches 476;

Petersen, Carolyn VENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, VENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS VENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM 41; LPPNSDTSKE-----TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 133 134 ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 193 Gaps 254 РТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТАРК 313 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 88 APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTT------194 TIIKSAPTIPKEPAPTITKSAPTIPKEPAPITIKEPAPTIPKEPAPTITKEPAPTITKSA 314 KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTT Indels 442; 7.4%; Score 489; DB 3; Length 1721; Similarity 22.1%; Pred. No. 7.8e-25; Conservative 82; Mismatches 476; Indels 44 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,361B 476; PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677 E: PETERS, VERNY, JONES & BIKSA 385 Sherman Avenue, Suite 6 SPECIES INFECTIONS Sequence 6, Application US/08928361B; Patent No. 6071518; GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE 12-SEP-1997 1721 amino acids TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: ; MOLECULE TYPE: protein US-08-928-361B-6 APPLICANT PETERSON,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: NUMBER OF SEQUENCES: COUNTRY: USA ZIP: 94306-1840 amino acid STREET: 385 Shere CITY: Palo Alto FILING DATE: 1 CLASSIFICATION: STRANDEDNESS ADDRESSEE: S US-08-928-361B-6 284; Query Match Best Local Si Matches 284; 29 89 159 209 엄 ò 8 ò g g à ò ò QQ

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IMKTPTQTDSVTGKPIDPTTGLPFNPPTGHLINPTNNTMDSSFAGAYKYAVSNGIKTDN 1023
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; Patent No. 5198535
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APPLICANT: Hoffman, Stephen I
APPLICANT: Charoenvit, Yupin
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374 PKE-
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649 416 654 444 PNKPNP----PSNPNKPNPN-----EPLNPNEPSNPNEPSNPNAPSNPNE--PSNPNE 492 476 TIPEEPIPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 534 273 TPCKVRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNN 332 443 594 192 IPTIIKSAPTIPKEPA-PITIKSAPTIPKEPA-PITIKEP----APTIPKEP-APITIKE 244 APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
TITLE OF INVENTION: Immunogen and gene
TUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: A. David Spevack
STREET: NARDC Building 1 T-12 National Naval
STREET: Medical Center
CITY: Bethesda
STREET: Wr. PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT PKEPI------NPEESNPKEP----INPEDNENPLIIODEPIEPRNDSNVIPI KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT 245 PAPITIKSAPIIPKEP-APIIPKKP-APIIPKEP-APTIPKEP-IPIIFKEPAPIIKEPA 301 PITPKEPAPIAPK--KPAPIIPKEPAPIITPKEPAPIIIKEPSPITPKEPAPITIKSAPIT 359 TKEPAPTITKSAPTTPKEPSPTTTKEPAPTTPKEPA-PTTPKKP-APTTPKEPAPTTPKE PAPITIKKPAPIAPKEP-APITPKETAPITPKKLIPTIPEKLAPITPEKPAPITPEELAP Length 826; Indels Query Match
7.4%; Score 488.5; DB 1;
Best Local Similarity 26.4%; Pred. No. 3.5e-25;
Matches 153; Conservative 54; Mismatches 223; CURKENI AFFLLIALIN NATA:

APPLICATION NUMBER: US/07/638,431
FILING DATE: 19910110
CLASSIFICATION: 424
ATTOKNEY/AGENT INFORMATION:
TELEPHONE: (301) 295-6759
TELEPHONE: (301) 295-6759
TELEPAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID ZIP: 20814-5044
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1:24
CURRENT APPLICATION DATA: , MOLECULE TYPE: protein US-07-638-431-2 USA TOPOLOGY: STATE: MI COUNTRY: 117 535 607 493 565 qq g δλ qq δ g δ g άy qq ŏ g QΥ

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S H S B BS	655 TPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE 708	SGULT 8 T. US92-00018-2 Sequence 2. Application PC/TUS9200018 Sequence 2. Application PC/TUS9200018 Sequence 2. Application PC/TUS9200018 Sequence 2. Application PC/TUS9200018 APPLICANT: Charcenvit, Yupin APPLICANT: Redestrom, Richard APPLICANT: Redestrom, Richard APPLICANT: Redestrom, Richard APPLICANT: Redestrom, Further and a pene encoding TITLE OF INVENTION: Protective malaria sporozoite surface protein NUMBER OF SEQUENCES: ADDRESSEE: A. David Spewack STREET: MARDC Building 1 T-12 National Naval CONFRES UNBOC Building 1 T-12 National Naval CITY: Bethesda STREET: Madical Center CITY: Bethesda CONFRY: USA CON	Secre 488.5; DB 5; Length 826;  1st Local Similarity 26.4%; Pred. No. 3.5e-25;  tches 153; Conservative 54; Mismatches 223; Indels 149; Gaps 34;  192 TPTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEPAPTTPKE-APTTTKE 244  273 TPCKVRDCPQIPIPPVIPNKIPERPSINDEEPVNRNDRNNPNNPNNPNNPNNPNNPNN 332  245 PAPTTKSAPTTPKEP-APTTPKEP-APTTPKEPTPTTPKEPAPTTKEPA 300  1
		RESULT PCT - US92; Sequer APP APP APP APP APP APP APP APP APP AP	Query Matches Matches Qy 192 Db 273 Qy 245 Db 333 Qy 301 Db 393 Qy 369 Ob 444

45; 476 TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 534 594 654 655 TPKEP-----APTTPKKPAPTTPETPPPTTSEVSTPTTKEPTTIHKSPDESTPELSAE 708 135 TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 190 75 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKE 134 191 PTPTTIKSAPT-TPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPA--P 247 248 TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTT----PKEPTPTTPKEPAPTTKEPAPT 302 303 TPKEPAPTAPKKPA--PTTPKEPA--PTTPKEPAPTTTKEPSPTTP----KEPAPTTTK 353 197 YP----PIYKAKPSYPPIYKAKPSYPPIYKAKPSYPPIYKAKPSYPSLIKAKPSYPPIYK 252 354 SAPITIKEPA-----PITIKSAPITPKEPSPITIKEPA--PITPKEPA----PITPKK 400 535 КGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT Indels 169; Query Match 7.3%; Score 476.5; DB 6; Length 652; Best Local Similarity 29.7%; Pred. No. 1.7e-24; Matches 221; Conservative 71; Mismatches 284; Indels 169. ; Patent No. 5202236

\*\*APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

\*\*ITILE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE 709 PIPKALENSPK------EPGVPTTK 727 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1997
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984 NUMBER OF SEQUENCES: 39 LENGTH: 652 SEQ ID NO:13: RESULT 9 5202236-13 265 595 41 80 PROTEIN ŏ g Сp δý QΥ qq δ QQ δ Dp ò QQ ö g ò g ò g δ

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PTTPKEPAPTTP - - - KEPTPTTPKEPA - - PTTKEPAPTTPKEPA
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-479-537A-5
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APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.S.
APPLICANT: BOUWSTRA, JAN B.S.
APPLICANT: BOUWSTRA, JAN B.S.
APPLICANT: WOORNER, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WIND, RICHELE D.
TITLE OF INVENTION: SILVER HALIDE ENULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE ENULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE ENULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULPREARTION THEREOF
TITLE OF INVENTION: PREPARATION THEREOF
SILVER OF INVENTION: PREPARATION THEREOF
SILVER OF INVENTION: PREPARATION THEREOF
SILVER OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: PREPARATION THEREOF
SILVER HALING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENTIN VEF. 2.1
SEQ ID NO 5
LENGTH: 960
TYPE: PDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPKAETTTKGPALTTPKEPTPTPKEPASTTPKEPTPTTIKSAPTTPKEPAP--TTTKS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPAGPPGSRDPG--PPGAPGPAGP--PGSRDPGAPG-PAGPPGSRDPGPPGAPGPA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APITPKEPAPITIKEPA-PTIPKEPAPITIKEPAPITIKSAPITPKEPAPITP----KKPA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 KPTYPSTYKAKPSYPPTYKPKISYPPTYKAKPSYPSTYKAKSSYPPTYKAKPSYPPTYKA 473
                                                                                                                                                                                                                                                                                                                                                            676 PPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPE 735
                                                                                                                                                             564
                                                                                                                                                                                                                                                              521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description of Artificial Sequence: Illustrative amino acid sequence
                                                                                                                                                                                                                                                                                              623 APKELAPTTKGPTSTISDKPAPTTPKETAPTTPKEPA--PTTPKKPA-PTT----PETP
                                                                                                                                                                                                                                                                                                                  401 PA--PTTPKEPA--PTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEK
                                               457 LAPTTPE--KPAPTTPEELAPTTPEEPT--PTTPEEPA-PTTPKAAAPNTPKEPAPTTPK
                                                                                                                                                           EPA-PTT----PKEPAPTTPKETAPTT--PKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
                                                                                                                                                                                                                                                    EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKGTAPTTLKEPA--PTTPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 960;
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25.6%; Pred. No. 1.2e-22;
Live 60; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621 YPPTHKAKPTYKAKPSYPPTHKAKP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                   736 MTTTAKDKTTERDLRTTPETTTAAP 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 25.6%
Matches 173; Conservative
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OTHER INFORMATION:
US-09-219-849-5
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Sequence 5, Application US/08479537A

Sequence 5, Application US/08479537A

Sequence 5, Application US/08479537A

Sequence 5, Application US/08479537A

Sequence 6, Application CIAMBON, Pierre

APPLICANT: LATHE Richard

APPLICANT: LATHE Richard

APPLICANT: LATHE Richard

APPLICANT: LATHE RICHARD

TITLE OF INVENTION: PRARMACEUTICAL COMPOSITION FOR THE

TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS: 5

CORRESPER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. BOX 1404 APTTPKKPAP-----KELAPTTTKGPTST--TSDKPAPTTPKETAPTTPKEPAPTTPKK 666 GP--PGAPGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGP--PGA 636 PAPTTP----ETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALEN----S 717 559 614 580 462 299 GPPGSRDPGP-----PGAPGPAGPPGSRDPGP--PGAPGPPGSRDPGP--PGAPGP 348 TTP---KEPAPTTTKKPA-----PTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTT 461 349 AGPPGSRDPGPPGAPGPPGSRDPGPPGAPGPAGPPGSRDPGP----PGAPGPAGPPG 404 354 SRDPGPPGAPGPPGSPDPGP--PGAPGPAGPPGSRDPGPPGSRDPGPPGSRDPGPP 517 TPKEPA-----PTTPKET-APTTPKGT-----APTTLKEPAPTTPKKP-APKELA 463 GAHGPAGPKGAHGPAGPKGAHGPAGPKGAHGPAGPKGAPGPAGPPGSKDPGPPGAPGPAG PPGSRDPGPPGA--PGPAGPPGSRDPGPPGAPGPPGPPGPPGPPGSRDP 462 PEKPAPT-TPEELAPTTPEEPTPTTPEEPAPTTPKAAA-PNTPKEPAPTTP---KEPAPT PTTTKEPTSTTSDKPAPTTPKGTA-PTTPKEPAPTTP---KEPAPTTPKGTA-PTTLKEP -----PTAPK-KPAPTTP---KEPAPTTPKEPA-PTTKEPSPTTPKEPAPTTTKS 245 PAGPKGAHGPAGPKGAPGPPAGPFGRDPGAPGPPGSRDPGP---PA APTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTP----KKPAPTTPKEPAP Patentin Release #1.0, Version #1.30 FILING DATE: 07-JUN-1995
CLASSIFICATION: 514 STATE: Virginia
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: 718 PKEPGVPTTKTPAATK 733 696 SRDPGPPGAHGPAGPK 711

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181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 240
                                                                                                                                          436
                                                                                                                                                                                                                     SAPDXRPYPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 419
                                                      ---APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        763 DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVEMPEVTPDMDYLPRVPNQGIIINPMLSD 966
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                                                                                                                  336 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT-----TKSAPTTPKEPSPTTK----E
                                                                                241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                      385 PAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                        437 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                                                                                                                                                                                                                                                                        420 SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                                                                                                                                                                                                                                                                                           493 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                                                                                                                            472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
                                                                                                                                                                                                                                                                                                                                                                                               548 TIP-----KKPAPKELAPITIKEPISTISDKPAP--ITPKGTAPITPKEPAPITP
                                                                                                                                                                                                                                                                                                                                                                                                                            531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                596 KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTKGPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          686 TTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848 KPIKAPKKPTSIKKPKTMPRVRKPKTTPTPRKMTSTMPELNPISRIAEAMLOTTTRPNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1021
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APPLICANT: CHAMBON, PIETRE
APPLICANT: CHAMBON, PIETRE
APPLICANT: LATHY, MATIE-Paule
APPLICANT: LATHY, MATE
APPLICANT: HARBUVENI, MATE
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR T
TITLE OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-083-116-5
; Sequence 5, Application US/09083116
; Patent No. 6203795
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "The amino acids spanning
128 to 1727 constitute a repeated region wherein the repeat
20 amino acids, 17 of which are fixed. The number of such
repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acid 134 is X1 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 P-KAETTTKGP--ALTTPKEP-----TPTTPKEPASTTPKEPTTIKSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----APTTTKEPAPTTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.5%; Score 424.5; DB 2; Length 1867; Best Local Similarity 23.7%; Pred. No. 1.8e-20; Matches 255; Conservative 69; Mismatches 511; Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acids 1 to 21 are a
21 amino acid precursor sequence."
                                                                                                APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MR-1995
ATTORNEY FAGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
     PCT/FR91/00835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPKEPAPITT-----KSAPTTPKEP------
                                MADER: US 08/039,320
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF TILING DATE:
FILING DAFF: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OR
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 128.1727
OTHER INFORMATION: //
OTHER INFORMATION: 12
OTHER INFORMATION: 15
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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INFORMATION:
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-479-537A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 147
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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OTHER INFORMATION:
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NAME/KEY:
LOCATION:
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Query Match 6.5%; Score 424.5; DB 4; Length 1867; Best Local Similarity 23.7%; Pred. No. 1.8e-20; Matches 255; Conservative 69; Mismatches 511; Indels 241; Gaps 53;	99 T	201	242 TKEPAPITTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT 288 :     :	289	7 336 TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE 384 :	385	y 437 TPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTPEEPAPT 492  1 :	493	548	596 586	OY 642 KPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP 685	OY 686 TTTKEPTTTHKSPDESTPELSAEPTPRALENSPKEPGVPTTKTPAA 731	732 -TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 	OY 788 TITODITERITILATION TITLAPKVITIKTITITEIMNKPEETAKPKDRAINSKATTPKPO 847  DD 821 APDXRPXPGSTAPXAHGVISAPDXRPXGSTAPXAHGVTSXPDXRPXP- 868  QY 848 KPTKAPKKPTSTKKPKTMFRVRKPTTPTFRKMTSTMPELNPTSRIAEAMLQTITPRNOT 907  DD 869 -GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPXPGST 911	908
	\to \fa	~ ~ ~	QY	VO OY	VO QU	ko da	ko da	ko da	λδ	wherein the repeat i The number of such		n Pro = CCT, CCC, CCA	.n Thr = ACT, ACC, ACA	in Pro = CCI, CCC, CCP	
4	ginia nnited States nable FORM: : Floppy disk IBM PC compatible yYSTEM: PC-DOS/MS-DOS YEATHIN Release #1.0, Version #1.30	A: US/09/083,116	08/479,537	WO PCIVEKSI/UU833 -1991 US 08/039,320	. US 08/403,576 1995	TION: L. 55,030 BER: 017753-025	KMALION: 6620 2021 0: 5:	CS: acids e	Ψ	/note= "The amino acids spanning 128 to 1727 constitute a repeated region 20 amino acids, 17 of which are fixed.	repeacs varios reas	r Ala w] 3CA, or	/note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn wherei or AGG; and Asn = AAT or AAC."	= Xaa Alawł CA, or	/note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
STREET: P.O. Box 1404 CITY: Alexandria	STATE: Virginia COUNTRY: United States ZIP: 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release	CURRENT APPLICATION DATA APPLICATION NUMBER: UFILING DATE: CLASSIFICATION:		TOMBER: 23-OCT- TON DATA: WUMBER:	FILING DAIE: 04 FEB 1550 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0 FILING DAIE: 14-MAR-1995	ATTORNEY/AGENT INFORMATION: NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:	TELECOMMUNICATION INFORMATION: TELEPRACE: (703) 836-620 TELEPRX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 5:	SEQUENCE CHARACTERISTICS: LENGTH: 1867 amino acids TYPE: amino acid STRANDEDNESS: single	TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE: NAME/KEY: Peptide	LOCATION: 1281727 OTHER INFORMATION: // OTHER INFORMATION: 1/ OTHER INFORMATION: 2/	FEATURE: NAME/KEY: Peptide LOCATION: 134	RMATION:	NAME/KEY: Peptide LOCATION: 144 OTHER INFORMATION: OTHER INFORMATION:	KEY: ION: INFO! INFO! INFO!	NAME/KEY: Peptide LOCATION: 121 OTHER INFORMATION: OTHER INFORMATION: S-09-083-116-5

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/note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 TTPKEPAPTTT-----KSAPTTPKEP-----APTTTKEPAPTTPKEPAPTT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 TSLIVNKETTVETKETTTTNKOTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKE--PAPTIKEP-----APTIPKEPAPTAPK----KPAPTIPKEPAPTIPKEPAPTT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT-----TKSAPTTPKEPSPTTK----E 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 P-KAETTTKGP--ALTTPKEP-----TPTTPKEPASTTPKEPTTIKSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTTKGPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KKPAPTTPETPPPTTSEVSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2035;
                                                                                                                                                                                                                                                                                                   /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 424.5; DB 2;
23.7%; Pred. No. 2e-20;
tive 69; Mismatches 511;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 23.7%
Matches 255; Conservative
                                                                                                                                                                                                                                                  NAME/KEY: Peptide
COCATION: 1.21
OTHER INFORMATION:
US-08-479-537A-2
                                                   OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
LOCATION: 147
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
  OTHER INFORMATION:
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Xaa Xaa which is the codon for Pro or Ala wherein Pro = CCT,
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The amino acids spanning
128 to 1899 constitute a repeated region wherein the
20 amino acids, 17 of which are fixed. The number of
repeats varies from 1 to 40."
                                                                                                                                                                                                               APPLICANT: KIENY, MATIE—PBULE
APPLICANT: LATHE, RICHARD
APPLICANT: LATHE, RICHARD
APPLICANT: LATHE, RICHARD
APPLICANT: HARBUVENI, MATA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
958 VTSAPDXRPXPGSTAPXAHGVTSA------PDXRPXPGSTAPXAHGVTSAPD 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/FR91/00835
FILING DATE: 23-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECOMUNICATION INFORMATION:
TELEPAN: (703) 836-6620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
                                                                                                                             Sequence 2, Application US/08479537A Patent No. 5861381 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION: 12
OTHER INFORMATION: 12
OTHER INFORMATION: re
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
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                                                                                                           US-08-479-537A-2
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821 APDXRPXPG-----STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
                                             763 DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
                                                                                                                                                                                                      848 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 907
                                                                                                                                                                                                                                                                                                         908 -PNSKLYEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 966
                                                                                                                                                                                                                                                                                                                                                          912 APXAHGVTSAPDXRPXPGSTAPXAH------GVTSAPDXRPXPGSTA----PXAHG 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 VTSAPDXRPXPGSTAPXAHGVTSA------PDXRPXPGSTAPXAHGVTSAPD 1003
                                                                                                                                                                                                                                                                                                                                                                                                             967 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HARBUVENI, MATA
APPLICANT: HARBUVENI, MATA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
732 -TKPEMTTTAKDK----TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                   TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                         869 -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIE: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    017753-025
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FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/083,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,537
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION UNDRER: 35,030
REFERENCE/DOCKET MUMBER: 01775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMCTH: 2035 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09083116
Patent No. 6203795
GENERAL INFORMATION: APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIENY, Marie-Paule APPLICANT: LATHE, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
COUNTRY: United States
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CITY: Al
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/note= "Amino acid 134 is X1 = Xaa
Xaa Xaa which is the codon for Pro or Ala wherein Pro = CC
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                       /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 IPKETAP----TIPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 P-KAETTTKGP--ALTTPKEP-----TPTTPKEPASTTPKEPTPTIKSAP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 РАРТТРКЕРАРТТРК----КРАРТТРКЕРАРТТРК----ЕРАРТТККРАРТАРКЕРАРТ 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 241; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.5%; Score 424.5; DB 4; Best Local Similarity 23.7%; Pred. No. 2e-20; Matches 255; Conservative 69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 TTPKEPAPTTT-----KSAPTTPKEP-
                MOLECULE TYPE: peptide
                                                              NAME/KEY: Peptide LOCATION: 128..1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: 1..21
COTHER INFORMATION:
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NAME/KEY: Peptide
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TTP-----KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 595
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                                                                                                                                                                                                                                                                                                                       103 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 762
                                                                                                                                                                                                                                                                                                                                                           732 -TKPEMTITAKDK----TTERDLRTTPETTTAAPKWTKETATTTEKTTESKITATTTQVTS 787
                                                                                                                                                                                                                                                                                                                                                                                               763 DXRPXPGSTAPXAHGVISAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
                                                                                                                                                                                                                                                                                                                                                                                                                                      788 TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                821 APDXRPXPG-----STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPXRPXP- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 APXAHGVISAPDXRPXPGSIAPXAH------GVISAPDXRPXPGSIA----PXAHG 957
                                                                                          531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                596 KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTTKGPTSTTSD
                                                                                                                                                                                                          KPAP--TTPK----ETAPTTPKEPAPTTP------KKPAPTTPETPPPTTSEVSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPTKAPKKPTSTKKPKTMPRVRKPKTTPFPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hardy, Daniel M.
APPLICANT: Hardy, Daniel M.
APPLICANT: Hardy Carbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES:
ADDRESSEE: ALDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
STREET: Houston
STREET: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUDIATE: U.S.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
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NAME: KIECHELL, BADDER S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION:
TELEPHONE: 713-789-1400
TELEFAX: 713-789-2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08276967
Patent No. 5851817
GENERAL INFORMATION:
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31; 546 APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPT-TPKEPAPTTPKEPAPTTPK 604 605 GTAPTILKEPAPTTPKKPAPKELAPT-TTKGPTSTT---SDKPAPTTPKETAPTTPKEPA 660 PKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATT 770 Gaps 513 VPTEKPIVPTEKHTIPTEKLTVLTERTTTPTERTTIPTEKPTVPTEKPSVPT-EKPTVPT 571 EKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTEIMNKPEETA 830 831 KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT 890 653 AP-----TTPQP-SPTLVPTQPAAVVMPST-----SATTVTPRTIASCP---PN 693 430 PKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTPEED 490 APTTPKAAAPNTPKEPA----PTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP PTTPKKPAPTTPETPPP----TTSEVSTPT-----TTKEPTTIHKSPDESTPELSAEPT ERTT-----TPIIRTTPTERTT---IPTKKTT-----VPTEKTIIPT-----ERTI Indels 119; Length 2476; 6.4%; Score 419.5; DB 2; 32.5%; Pred. No. 5.5e-20; tive 43; Mismatches 177; Search completed: April 26, 2002, 16:25:14 Job time: 454 sec SRIABAMLQTTTRPNQTPNSKL 912 : : ||| :| AHFERCACPVSCQ-SPTPNCEL 714 TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear Query Match
Best Local Similarity 32.5%
Matches 163; Conservative TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-276-967-2 661 771 694 ò 임 δ g g ά g ò q ŏ 음 ò

Page 1

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

 protein search, using sw model OM protein

Run on:

April 26, 2002, 16:30:58; Search time 114.61 Seconds (without alignments) 905.906 Million cell updates/sec

Perfect score: Sequence:

AA2 7276 1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWYNCP 1363

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_68:\* 1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	and hor in the state of the sta	hypothetical prote hypothetical prote hypothetical prote gene Lf3 protein larval glue protein hypothetical protein hydroxyproline-ric hydroxyproline-ric neurofilament trip
SUMMARIES ID	A43932 1718262 1718262 1718262 1718251 176251 1718535 1718535 1718535 1734513 1734513 171622 1729757	F75518 729018 8729023 850125 850125 82456 822456 823760 8737 806733
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Length	3020 1664 1274 1274 2187 1186 1187 1129 1129 1344 3570 3570 3570 3507 489 761	839 801 924 379 2232 1630 350 875 875 620
% Query Match	11111111111111111111111111111111111111	
Score	1077 86.950 84.6 84.6 812 803 684.5 666.5 666.5 663.5 633 632 632 632 632 632 632 632	622.5 607.5 607.5 607.5 591.5 558.5 559 551 551
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calphotin - fruit hydroxyproline-fic hydroxyproline-fic extensin precursor neurofilament tilp hypothetical prote exo-alpha-sialidas calcium-binding pr hydroxyproline-ric neurofilament trip membrane glycoprot hypothetical prote tegument protein mucin-like glycopr
A47283 S220500 T32271 J00465 J00465 J00465 J006985 J000985 J000985 J145462 T45462 T45463 T45463
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873 369 1459 1459 1072 756 813 1162 854 854 866 11611 3534 1832
545 540 540 540 540 530 530 530 530 521 521 518 518 515 515 513
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

RESULT

	tinal - human (fragments)	SMUC-41	(man)	C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #+oxt change of variation	C, Accession: A49963; A45106; B45106; A43932; R33532; A51757; PA45430; PA4543	Rigum Jr., J.R.; Hicks, J.W.; Toribara N W . Siddit B. V	-2446, 1994	A.Title: Molecular cloning of human integring musto where	53; MUID: 94132002				21998	J.W.: Toribara, N.W.: Pothe F.W.: Texas	J. Biol. Chem. 267, 21375-21383, 1992	A, Title: The human MUC2 intestinal much has contesting the human MUC2 intestinal
A43932	mucin 2 precursor, intestinal - human (fragments)	N; Alternate names: mucin SMUC-41	C;Species: Homo sapiens (man)	C; Date: 10-Mar-1993 #sequence	C; Accession: A49963; A45106; E	R; Gum Jr., J.R.; Hicks, J.W.;	J. Biol. Chem. 269, 2440-2446, 1994	A; Title: Molecular cloning of	A; Reference number: A49963; MUID: 94132002	A; Accession: A49963	A; Molecule type: mRNA	A; Residues: 1-639 <gu1></gu1>	A; Cross-references: GB: L21998	R; Gum Jr., J.R.; Hicks, J.W.;	J. Biol. Chem. 267, 21375-2138	A; Title: The human MUC2 intest

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im, Y.S.

A; rittle: The human MUC2 intestinal mucin has cysteine-rich subdomains located both up A; Recence number: A45106; MUID:93016075
A; Accession: A45106
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 626-1895 cdU2>
A; Cross-references: G18-M94131; NID:9186395; PIDN:AAA59163.1; PID:9186396
A; Accession: B45106
A; Accession: B45106
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 2037-3020 cdU3>
A; Residues: 2037-3020 cdU3>
A; Cross-references: C18-M94131; NID:9186396
A; Cross-references: G18-M94131; NID:9186396
A; Cross-refe

Across-treferences: CB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398
A;Experimental source: colon
A;Experimental source: colon
A;Experimental source: colon
A;Experimental source: colon
B;Toribara, N.W.; Gum Jr., Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, J. Clin. Invest. 88, 1005-1013, 1991
A;Title: NUC-2 human small intestinal mucin gene structure. Repeated arrays and polym A;Reference number: A43932; MUID:91358717
A;Reference number: A43932
A;Residues: 1343-1350, L.,1352-1411, S',1413-1448, P',1450-1503, T',1505-1915 <TOR>A;Residues: 1343-1350, L.,1352-1411, S',1413-1448, P',1450-1503, T',1505-1915 <TOR>A;Cross-references: GB:M74027; NID:918863; PIDN:AAA59975.1; PID:918864
A;Note: sequence extracted from NCBI backbone (NCBIR:55749, NCBIP:55750)
B;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evi

A; Molecule type: mRNA A; Residues: 1916-2193 <GU4> A; Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874 A; Experimental source: intestine R; Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

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encoding the cellulo
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C;Species: Clostridium thermocellum
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2215
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                                                                                                            1742 TIMITLPPITISSPLITIPLPPSIIPPIFSPFSIITPTIPCVPLCNWIGMLDSGKPNFHK 1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1919 LOAPTPTPISTITIVTPTPTFTGTQTPT-TTPITTTTTTTTTTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                     1862 PMAFCLNYEINVQCCECVIOPTIM---TITITENPIPIPITTTTTTTTTTTTTTTSTGSPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKGPTST-TSDKPAPTTPKETAPTTPKEPAPTTPKKP-----APTTPETPPPTTSEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 IPTTK-----EPTIIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTT
                                                                                                                                                                                                                                                                                                  1802 PGGDTELIGDVCGPGWAANISCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQKPGGVI
                                                                                                                                                                                                                                                                                                                                             ---TAPTTLKEPAPTTPKKPAPKELAPTT--TKEPTSTTSDKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                --APT-TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT
TITKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPK
                           ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fujino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
A;Title: Organization of a Clostridium thermocellum gene cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 950; DB 2;
Pred. No. 1.5e-32;
                                                                                                                                                                             NTPKEPAPTTPKEPAPTTPKEPAPTTP-----KETAPTTP-
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A;Accession: T18262
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A; Residues: 'T', 1925-1948, TTS', 1952-1954 <JAN>
A; Residues: 'T', 1925-1954, TTS', 1952-1954 <JAN>
A; Residues: 'T', 1925-1954, TTS', 1952-1954 <JANS
B; Xb, G; Huntal source: bronchus
B; Xu, G; Huntal intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-th
A; Title: Hunnan intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-th
A; Reference number: PQ0328; MUID:92198477
A; Residues: 2328-2468 <XUG>
A; Residues: 2328-2468 <XUG>
A; Residues: 2328-2468 <XUG>
A; Experimental source: small intestine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat C;Superfamily: von Willebrand factor; tandem repeat C;Keywords: glycoprotein; intestine; tandem repeat F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFERGRECDC-----DAQCKKYDKC-----CPDYESFCAEVHNPTSPPSSKKAP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVVDEAGSGLDNGDF---KVTTPDTSTTQH----NKVSTSPKITTAKPINPRPSLPPNSD
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                                               mucin gene
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14.8%; Score 1077; DB 2; Length 30
Best Local Similarity 27.2%; Pred. No. 1.4e-37;
Matches 373; Conservative 103; Mismatches 497; Indels
                    J. Clin. Invest. 87, 77-82, 1991
A; Title: Human bronchus and intestine express the same A; Reference number: A61257; MUID:91086481
A; Accession: A61257
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1197 PPGASVPTEETCKSCVCTNSSQVVCRPEEGK-
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A; Residues: 2328-2342,'K', 2344-2354 <XUG1>
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                                                                  KPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP
                                                                                                        TIPKEPA--PITIKEPSPI-TPKEPAPITIKS-APITIKEPAPI----TIKSAPITPKEPS
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     230;
    Indels
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  Mismatches 361;
Conservative 104;
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312;
Matches
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RESULT T31108

 Phytophthora infestans 51; TKKVIESEEITEEHSVSENQESSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNK 163 454 315 372 422 629 ETIYAPTEETMYAPIEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTY 1047 PKEP-----APTAPKKPAPTTPKEPAPTTPKEP-----APTAPKKPAPTTPKEPAP 459 603 867 ETTYAPTEETPYEPTEETTYAPTKETTYAPTEETTYASTEETTYAPTEETTYAPAEETPY 927 695 -----TLKEPAPTTPKKP-----APKE---LAPT--TTKGPTSTTSDKPAP 779 TPTVGYSTEETEGOHVTGGYEPSDETEAPTEGTTY--VPREETTAAPSE-----DTTYAP KNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTT-----QHNKVSTSPKITTAKPI : | || || : : | :| || REVTPYAPIEKPYDVEETTYVTEESTYAPIKSETNAPTERMHYAHIEKPCDIEVTMYAPT NPRPSLP---------PNSDT----SKETSLTVKETTVETKETT---TNKQT STDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTTPK EPASTTPKEPTPTIKSAPTTPKEPAPT-TTKSAPTTPKEPAPT--TTKEPAPTTPKEPA 373 PTTTKEPAPTTTKSAPT-----TPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTT 571 BETTYAPTEETT-YAPTEETMYAPIEETTYAPTEETTYAPAEETPYRPTEET 630 TYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAP TTPKEPAPT--TTKEPSPTTPKEP-----APT-TTKSAPT-----TTKEP----T--TPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTT --APT-TTKSAPT--TPKEPSPTTTKEP-----APTTPKEPAPTTPKKPAPTTPKEPAP PEELAPT--TPEEPTPTTPEEP-----APT------TPKAAAPNTPKEPAPTTPK EP-----APTTPKEPAPTTPKETAPTTPKGTAPT--TLKEPAPTTPKKPAPK-ELAPT--TTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEP----APTTPKGTAPT----229; Length Indels Query Match
11.9%; Score 863.5; DB 2;
Best Local Similarity 31.7%; Pred. No. 5.3e-29;
Matches 368; Conservative 55; Mismatches 509; 104 282 164 218 335 256 316 423 546 460 069 497 868 504 646 928 969 988 744 QQ ò ò g ò Ω ò g ò g ò g a ò δ Ω à QQ g ò g g δ ŏ à g

	0.0   0.76   LKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPT	RESULT 5 T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse N; Alternate names: alpha-NAC protein C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Accession: T30826 R; Yotov, W.V.; St-Arnaud, R. Genes Dev. 10, 1763-1772, 1999 A; Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a mus A; Reference number: 220889; MUID:96312450 A; Accession: T30826 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-2187 < VOT>
Db 1048 ASTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAPTE 1107  OY 780 TTPKETAPTTPKEPAPTTPKKPAPTTPETTYAPTEETTYAPTEETTYAPTE 1107  Db 1108 ETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYGPTEETTY	RESULT 4 T16251 T16251 T16251 T16251 T16251 T16251 T16251 T16251 T16251 Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 20. Sep-1999 #text_change 18-Feb-2000 C; Date: 20. Sep-1999 #text_change 18-Feb-2000 C; Date: 20. Sep-1999 T16251 R; Leimbach, D. R; Reference number: 218485 A; Recession: T16251 A; Recession: T16251 A; Recession: T16251 A; Recession: T16251 A; Residues: DNA A; Residues: DNA A; Residues: 1-1274 A; Leimbach DNA A; Residues: 1-1274 A; Molecule type: DNA A; Molecule	245 245 174 295 229 355 289 415

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                              A Map position: 10
A:Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A:Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding active: Keywords: alternative splicing; DNA binding; transcription factor
                                                                                                                                     51;
EMBL:U48363; NID:g1666688; PID:g1666689; PIDN:AAB18732.1
                                                                                                                                                                                                                                                                                                                                                                                                           998 PEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKRAPKTAVSKEIPSKGVTAVPLEISLP 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1293
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                                                                                                                                                   68 NPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSS 127
                                                                                                                                                                              -----PPSPKGAPIVPTESSISSKQVPAEILPSPQ 792
                                                                                                                                                                                                   SSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDN 187
                                                                                                                                                                                                                                                          240
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                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                         -----DISATLSLKSVPAVTSLSPPKAPVAPSNEATIVPTEIPTSLKNALAAATPKE
                                                                                                                                                                                                                                                                                                                T-----TVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKA
                                                                                                                                                                                                                                                                                                                                                                ------EPAPTTKEPAPTTPKEPAPTTTKEPAPTT---TKSAPT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 PAPTAPKKPAPTT--PKEPAP----TTPKEPAPTTTKEPSPTTPK-----EPAPTTKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAASSQKRSPKTSVPKETPPGGVTAMPLEIPSAPQKAPKTAVPKQIPTPEDAVTILAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTTKEPAPTTT-KSAPTTPK-----EPSPTTTKEPAPTTPKEPAPTTPKKPAPTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PKE------PAPTTPKEPAP-----TTTKKPAPTAPKEPAPTTPKETAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1348 IPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIPPSPRKGSKKAGSKE-TPTTPSPEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TISDKPAPTIPTEPTS-----TISDKPAPTIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPEEPTPTT-----PEEPAPTTPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631 AAPNTPKEPAPTTPKE-PAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPTIPKE-PAPTIPKGTAPITLKEPAPTIPKKPAPKELAPITIKGPISTISDKPAPTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KETAPTTPKEPAPTTPKKPAPTTPETP-----PPTTSEVSTPTTK-----EPTTIHKS
                                                                                                                                     246;
                                                                                                                                                                                                                         KTPEVTASRLISAVQSPKVDPIMSD-----VTPTSPKKTSATAVPK------
                                                                                                             Length 2187;
                                                                                                                                   449; Indels
                                                                                                       11.2%; Score 812; DB 2;
27.4%; Pred. No. 1.1e-26;
1ve 128; Mismatches 449;
                                                                                                                                  Conservative 128;
                                                                                                                                                                             SPT-PPSSKGAPVPSTGA----
                                                                                                                    Similarity
A; Cross-references:
                                                                                                      Query Match
Best Local Simil
Matches 311; C
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Ni-Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR01 C;Species: Saccharonyces cerevisiae C;Date: 10-can-lone acceptance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. Alternate names: attracellular glucoamylase; mucin-like protein MUC1; protein v C. Species: Saccharomyces cerevisiae
C. Date: 10-26p-1999; sequence_revisiae
C. Date: 10-26p-1999; sequence_revision 10-Sep-1999; #text_change 12-Nov-1999
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                                             PDESTPELSAEPTPKALENSPKE-PGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETT
                                                                                                                                                                                                 ITTTEIMNKPEETAKPKDRAINSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPT
                                                                                                                                        TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKT
                                                                                                                                                                                                                                                                                                                                  | : |:||: |:||
STAPSLEGAPKETSE---TSVSKVLMSSP-----PKKASSSKRASTLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                             1011 PRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETP 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.1%; Score 809; DB 1; Length 1367; Local Similarity 27.5%; Pred. No. 9e-27; nes 328; Conservative 112; Mismatches 526; Indels 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 328,
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832
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1013 -----NSAGETTSGC 1109 902 ----TKAPKKPTSTKKPKTM 999 894 677 KEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAP---TTPKEPA 733 792 PITPKEPSPITIKEPAPITPKEPAPI-IPKKPAPITPKEPAPITPKEPAPITIKKPAPIA 563 611 622 463 444 512 504 340 407 387 314 DCDAQCKKYDK----CCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPN 100 PT-TPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKE PVPTPSSSTTESSSAPVPTPSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSTESSSV 903 TTEKTTESKITAT--TTQVTSTTTQDTTPFKITTLKTTTLAPKVTT---TKKTITT-EI 954 TISGCSPKTVTTVPTTTTTTSVTTSSTTTITTTVCSTGINSAGETTSGCSPKTITITTVPC PRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGA 793 PAP----TTPKKPAPTTPETPPPTTSEVSTPT-----TTKEPTTIHKSPDESTPELSAE 843 PTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETAT APTT-----TKSAP----TTPKEPAPTTTKEPAPTTPKEPAP----TTTKEPAPTTTKSA PTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSA PAP----TTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPT-TPKGTAPTTL 408 APVISSTIESSSAPVISSTIESSSAPVTSS----TIESSSAPVTSSTIESSSAPVPTPSS 388 PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP----TTPKEPAPTTKEPAPTTPKEPAPT 445 APKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSA -----PTPSSSTTESSSAPAPTPS---SSTTESSSAPVTSS---TTESSSAPVPTPSS PKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT-TPEEPTPTTPEE PTTTSCTKEKPT--PPHHD-----TTPCT-----KKKTTTSKTCTKKTTTPV **APTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTKSAPTTPKEP** APV-----PTPSSSTTESSSAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSS 174 DESTGCNNYDNGGHSQTDFPGFFWNIDCDNNCGGTKSSTTTSSTSES--STT-----DNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPR PSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDL KKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVK MNKPEETAKPKDRATNSKATTPKPQKP--------1000 1066 505 778 719 612 623 299 734 564 191 221 315 281 354 341 464 513 101 224 275 44 g δ g g Ωý g ōλ qq οy Oy Db q δý Ω Qγ Dp Qγ g οy g Dp Οy OD ٥y

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33; cypecies: Zea mays (maize cypecies: Zea mays (maize) cypecies: Zear: 1955 #sequence\_revision 12-May-1995 #text\_change 29-Oct-1999 (CyAccession: S49915 R. Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A. submitted to the EMBL Data Library, June 1994 A; Description: Pex genes: pollen-specific genes with extensin-like domains. A; Reference number: S49915 A; Reference number: S49915 A; Accession: S49915 A; Accession: S49915 A; Residues: Lula Relus Carastales Preliminary A; Molecule type: DNA A; Residues: Lula Relus Caross-references: EMBL: Z34465; NID: 9600117; PIDN: CAAB4230.1; PID: 9600118 675 LKE---PA-----PITPKK---PAPKELAPTTKE---PISTTSDKPAPTTPKGTAPTTP 721 827 449 EGETPHMLLRPHVEMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNG 1119 171 PIPKPPVVDEAGSGLDNGDFKVTTPDISTTQHNKVSTSPKITTAKPINPRPSL----PPN 226 460 PTPHSPPAD------DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ 510 286 341 Gaps ----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPA PAPLSSPPAPQVKSSPPPVQVSSP-PPAPKSSPPLAPVSSPPQVEKTSPPPAPLSSPP PTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK **EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTTPKEPAPTTTKKPAPTAPKEPAP** TTPKETAP----TTP----KKLTPTTPEKLAPTTPEKPAP-----TTPEELAPTTPEEPT SP---KSEPVSSPPQTP----KSSPPPPAPVSSPPALAPVSSPPALAPVSSPPSVKSSP---PTTTKSAPTTP--KEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP-KEPAPTT PKKPAPTTPKEPAPTT-----PKE---PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKP SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 511 APVG----SPSPPPPVSVV SPPPPVKSPPPARVGSPPPPBKSPPPPARASPPPVKSPP--PPPTLVASPPPVKSPP 1110 SPKTVTTTVPCSTGTGEYTTEATTLVTTAVTTTVVTTESSTGTNSA-GKTTTGYTTKSVP TLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPIDTVFTRC----NCEGKT 1167 Length 1188; Indels 10.8%; Score 784; DB 2; L 29.9%; Pred. No. 8.6e-26; ive 59; Mismatches 359; 59; Mismatches Query Match 10.83 Best Local Similarity 29.93 Matches 230; Conservative 919 944 691 570 617 542 009 399 450 719 510 287 342 099 227 1120 1169 1060 ΩD a g QΥ qq QΥ g δλ g pp Οy Qγ QΥ pp Óγ QQ ò qq QΥ Ω δÿ ò QQ QΥ g

Db 582 TAQMVTQLAATKPSPIVPKASPK-ALMTPPPPPPGLPRALAAAKLLGLPSSPVASAMHAK 640  Qy 613EEPTPTTPEEPAPTTP		HEBULT 9  TASSOLT  Hypothetical protein F16F9.2 - Caenorhabditis elegans C, Species: Caenorhabditis elegans C, Species: Caenorhabditis elegans C, Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 R; Fulton, B. Submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmid F16F9. A; Reference number: Z20071 A; Reference number: Z20071 A; Reference number: Z20071 A; Reference number: DNA A; References: EMBL: U67956; PIDN: ABB07691.1; GSPDB:GN00028; CESP:F16F9.2 A; Experimental source: strain Bristol N2; clone F16F9 A; Gene: CESP:F16F9.2 A; Map position: X A; Introns: 35/1; 36/1/: 384/1: 482/2: 517/1: 071/1: 1001/2: 1102/2.	ore 684.5; DB 2 ed. No.1.2e-21; Mismatches 406 SCKG-RCFESFERGRE :     : : : : : : : : : : : : : : : : :
Oy 781 -TPKETAPTTPKEPAPTTPKKPAPTTSEVSTPTTTKEPTTIHKSPDESTPEL 839  1	Ouery Match.  9.6%; Score 695; DB 2; Length 1151; Best Local Similarity 25.3%; Pred. No. 4.2e-22; Matches 304; Conservative 108; Mismatches 466; Indels 324; Gaps 59;  Qy 64 AEVHNPTSPPSKKAPPPSGASQTIKSTTKRSPKPPNKKTKKVIESEEITEEH 117	EAKA ASLM PAPT DLPK PTPT I I I STGT KEPS	

ογ	61 8	FCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVS 120    I
a ò		NQESSSSSSSSSS
; q	4	::   ::   ::  ::   ::   ::   ::   ::
yo 4	181 A	AGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTA-KPINPRPSLPPNSDT 229  :
a č		SKETSLTVNKETTVETKETTTTNKOTSTDGKEKTTSAKETOSIEKTSAKDLAPTSKVLAK 289
Dp	170 5	
οy	290 E	PKAETTTKGPALTTPKEPTTTFKEPASTTPKEPTTIKSAPTTPKEPAPTTTKSAP 3 :
qq	229	97 1
QY	0	
ΩD	268	KAPATTEEPTPTTTEEVTTTEAETSTTTSSETSTEKPTTPLLDNKIAGFA 3.
δλ	up o	TPKEPAPTTPKEP - TPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKKEVAPTTPKKE 404
Op	ת	PVIGITY FDIALITY TAXABLE TO THE TAXA
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ò	σ	KEPSPTTTKEPAPTTPKEPAPTTPKKPAP537
연	33	 EETTTKSHVVPKPTKKGTVKVTPKLELSF
δy	538	-TTTKKPAPTAPKEPAPTT
qq	492	55
οy	572	EEPAP 
ф	552	EKTS 60
QY	626	<b>6</b> 0
Ω	605	
οy	989	-TTPKGTAPTTPKEPAPTTPKGTA
ορ	929	IITTDEETTSTTSTTPEITSTKEIVTESALT /0
ΟŊ	742	ILKEPAPTTP
qq	707	76
Qy	770	81
qq	767	E3
Qy	820	TITKEPITIHKSPDESTPELSAEPIPKALENSPKEPGVPTTKTPAATKPEMITTAKDKIT 87
QQ	827	TITSEPSTTESTTESTTTT
QY	880	ERDLRTTPETTTAAPKMTKET 90
qq	860	SAETSETTTSESAAFITGESPENTALQSSSQKSEENESSAEKPGARRDFVPKKHKTT 91.
ΟŸ	901	ATTTEKTTESKITATTTQ-VTSTTTQDT7PFKITTLKTTTLAPKVTTTKKTLTT 95
qq	917	VKPAETTSAVAASTTTTEPITTTEKSTTLETTPIEATTLNEVTGPAFVTGAPVDETTINT 9/
Qy	954	TEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKP 996

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in charge of muscle ultrastructure and elasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:91017426; PIDN:CAA62189.1; PID:91017427
                                            HMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETN 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APTTPKGTAPTTLKEPAPTTP------KKPAPKEL 692
РАТТРКЕТАРТТРККСТРТТРЕКСАРТТРЕКРАРТТРЕ- 605
                                                                                                          TPKGTAPTTPKEPAPTTPKEPAPTTPKG----TAPTTLK 746
                                                                                                                                                          PKELAPTTTKGPTSTTSDKPAP--TTPK----ETAPTTP 790
                                                                                                                                                                                                                                      vision 29-May-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                      PGVPTTKTPAA-----TKPEMTTTAKDK---TTERD 882
                                                                                                                                                                                                                                                                                                   TKETATTTEKTTESKITATTTQVTSTTTQDTTP--FKIT 933
                                                                                                                                                                                                                                                                                                                                                       --EIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.2%; Score 666.5; DB 2; Length 7962;
Best Local Similarity 24.2%; Pred. No. 4.4e-20;
Matches 268; Conservative 120; Mismatches 491; Indels 229; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGHYFWMLSPFSPPS 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d from GB/EMBL/DDBJ
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50;

Qy	57	PDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKK 102  :
٥y	103	KTKKVIESEEITEEHSVSENQESSSSSSSSSTIWKIKSSKNSAANRELQKKLKVK 160 :
ga Að	161	VTTP-DTSTTQHNKVSTSPKITTAKP-
qq	9869	:               : : :
Qy	217	-INPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKE 261 
δŏ	262	
qq	7056	EEGEFHEVEEFIKLEQHRVEEEHRVEKVHRVIEVFEAEEVEEKPRAPPKG 7107
ΟŊ	301	PALTTPKEPTTTP-KEPASTTPKEPTPTIKSAPTTPKEP-APTTTKSAPTTPK 353
Op	7108	TKVFEVLFFR
Oy Dp	354	EDAPTITKEPAPTIPKEPAPTITKEPAPTITKSAPTIPKEPAPTIFKKPAPITKE 4U9
ŏ	410	IPKEPTPTTPKEPAPTTKEPAPTTPKEPAP
o q	7214	:    ::
δλ	463	PAPT 522
QQ	7273	73
Qy Ph	523	TPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKK 582
ζō	583	LTPTTPEKLAPTT-
QQ	7380	:
QY	634	NTPKEPAPTTPKEPAPTIPKEPAPTIPKETAPTIPKGTAPTILKEPAPTT 683
qq	7438	
οy	684	PKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPT 743
g	7491	YEEPERIAPEEELAPEEERPVPVAEEEEFVFFFAVFELANTELENNATEROOF
Qy	744	TLKEPAPTTPKRAPKELAPTTINGPISIISDKRAPIIIRDIA 11:1
3 8	797	TPKKPAPTTPETPPPTT
경	7598	:   NPQVPE
Qy	846	KALENSPKEPGVPTT
q	7654	KKLE-KVKKPAVPEPPPPKPVEEVEVPTVIKKEKAIPEPINVFEINFAIFLERIA
92	902	<pre>? TITEKITESKITATITQVISTITQDITPRKITTLKITITLAKVITTTKYILITITEIMN 509 PKPA</pre>
3 8	046	PEFTAKPKDRATNSKATTPKPOKP
ž ć	7746	AKA

December   December
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GHYFWMLSPESPPSPARRITEVWGTPSPTDTVFTBCNGECKT 1167	1126	٠,
TALTPPVWISTTTTPTTTTPTTSGSTVTPSSIPGTTHTARVLTTTTTVATGSM 3280	322	
MLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDC	1066	~
TPSSTPETVHTSTVLTTTATTTGATGSVATPSSTPGTAHTTKVPTTTTTGETATPSSS	3167	0
STMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNDKSEDAGGAEGETBH 106	/ 1016	~
6 APKKPTSTKKPKTMPRVRKPKTTPTPRKMT	у 986 b 3107	~~~
TASTGSTATLSSTPGTTWILTEPSTTATVTAPP	304	• •
TLAPKVTTT-KKTITTTEIMNKPEETAKPKPDATTNSVATTTOND	у 939	<u> </u>
ETATTTEKTFESKITATTTQVTS-TTTQDTTPFKITTTLKTT 938	y 899 b 2987	~ 3
 	292	~
TPAATK	)у 862	~
O LTTTATTTASTGSTATE	N	~ :
VSTPTTTKEPTTIKSPDESTPET SAFETERAT ENCORPERATESTAMPSSTPGTTWILTE 2		~
CSLDFGLVCRNREOVGKFKMCENVETEOVECONVCCTORTE	)b 2810	
AWSEWLDY	275	, ,
793		
ESPPSPGTTTPGHTTATSRTTATATPSKTRTS	269	, 0
PKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEP 793	Ду 753	- 10
SPSSPHTVRTAWTSATSGTLGTTHITEPSTGTSHTPAATTGTTTTSTPALSSPHPSSRTT 26	Db 2634	
APTTPKEPAPTTPKEPAPTTPKGTAPT-TLKEPADTT 752	Qy 717	0
6 STTNPSSTPGTTPIPPELTTTATTPAATSSTVTPSSALGTTHTPPVPNTTATTHGRSL 26	Db 257	_
3 PTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTPKGT 716	Оу 67	$\sim$
6 TS	251	
C FERRETTENIES VALESSTEGTAHTIK V PITTTTGET VTPSSSPGTARTPPVWISTTT	ו ת	~ .
bTTPEKLAPTTPEKPAPTTPEELAPTTPEEP	UY 58	_ ~
6 LPALRSTATTPTATS	. 23	_
8 KPAPTAPKEPAPTTPKETAPTTPKKLT	vı	_
2 TTTATTTESTGSTATPSSTQGPPAGTPHVSTTATTPTVTSSKATPFSSPGTATA 2	23	
8 PTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTK 557	Оу 49	_
STPATSSTATPSSTPGTTWILTKL 2	Db 228	
5PTTPKEPAPTTTAKSATTTT	Оу 47	
*/* 22 WSEWLDYSYPMPGPSGGDFDTYSNIRAAGGAVCEQPLGLECRAQAOPGVPLRELGOVVFC 228	Db 22:	
75 474	Oy 4:	

	EPAPTTPKK 686     TTKPLTKLS 643	627 TPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKK :	Оу 6 5	
	TTPEEPAPT 626 ::  : :SSEDEKKS 590	OO/ PAPTTPEKETAPTTPEKLTPTTPEKLAPTTPEEKAPTTPEELAPTTPEEPTPTTPEEPAPT   :   : : : : : : : : : : : : : : : :	Db 5	
	KPAPTAPKE 566       : AKTTPAK 557			
	TTTKSAPTT 507   PGTPKTSAA 508			
	KEPAPTAPK 447    -   KTSTAKKDS 448			
	PAPTTTKSAP 388   :  : PAKKASSSSD 390			
	(SAPTTPKEP 340  : :    (AETSTDSES 339	85KVLAKPTPKAETT	,	
	AKDLAPTS 284          PPTSVS 279	22/ SUTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTS		
	INPRPSLPPN 226    TPP- 224	QPVI QPVI		
	RTKK 169 :    SSEDEASKKK 176			
	KKVIESEEITEE 116    :::::::: KPVVKAVQPKKA 116	SPESKKAPPENGASQTIKSTTKRSPKPPNKKKT    :  :    :  :  :  :  :  :  :  :  :  :	D 49	
40;	h 990; s 199; Gaps	G E	Ques Best Mato	
		rds: xNopp180 family: nucleolus-cytoplasm shuttle phosphoprotein rds: phosphoprotein	** ** ** **	
	1; PID:q895921	reliminary; translated from GB/EMBL/DDBJ type: mRNA 1-990 <cal> erences: EMBL:X88927; NID:9895920; PIDN:CAA61368.</cal>	A;Sta A;Mol A;Res A;Cro	
ein, xNopp	lar phosphoprotein,	J. Cell Sci. 108, 3339-3347, 1995 A;Title: Identification and cDNA cloning of a Xenopus nucleolar A;Reference number: IS1618; MUID:96019267 A;Accession: IS1618	J. Ce A;Tit A;Refi A;Acc	
	ınge 24-sep-1999	ISSOUR 13 ISSOUR 13 ISSOURCE IN THE PROPERTY OF THE PROPERTY ISSUED IN ISSUE	IS1618 IS1618 INCLEO C;Speci C;Date C;Acces	
		22	Db	

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TVSSTPSESSSEAPLTSSPATTTEVITESSVKSTTPKEESSSEITVKLSS 2085	TPSESS	Db 2	
KQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTP	238 NKETTV-ETKETTTTNKQTSTDG	Qy :	
ATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSESPEVSTSS 2025	8	_	
SGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTV 237	181 AGSGLDNGDFKVTTPDTSTTQHN	0y 1	
ENQESSSSSSSSSTIWKIKSKNSAANRELQKKLKVKUNNNNKIKNNFIFFFFFFFFFFFFFFFFFFFFFFFFFFF	121 ENQESSSSSSSSSSSTIWKIKS :: :   :  1952 IDEENSSSSNSG	Qy 1 Db 19	
	913	Db 19	
SFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVS 120	61 SFCAEVHNPTSPPSSKKAPPPSG:	Qy	
QELSCKGRCFESFERGRECDCDAQ	25 853	Qy Db 18	
8.7%; Score 636; DB 2; Length 3507; 22.6%; Pred. No. 3.6e-19; 1ve 173; Mismatches 459; Indels 296; Ga	Match 8.7%; Local Similarity 22.6%; es 271; Conservative 17	Query Best   Match	
1/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2;	Sp:zK783.1 tion: 3 14/1; 48/2; 84/1; 196	Gene Map Intr	
FAV> EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1 EM: strain Bristol N2; clone ZK783	: 1-3507 . : 1-3507 . ferences: ntal sources:	A; MOLECULE A; Residues: A; Cross-ref A; Experimen	
y; translated from GB/EMBL/DDBJ	n: T34513 preliminary; translated	A; Accession A; Status:	
n, M. SL Data Library, August 1994 sequence of C. elegans cosmid ZK783. Z21536	the EMBL Data n: The sequence number: Z21536	R; Favello, submitted A; Descript A; Referenc	~ ~ ~ ~
<sub>1</sub> ZK783.1 - Caenorhabditis elegans ditis elegans #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999	protein ZK783.1 - aenorhabditts elega ct-1999 #sequence_r T34513	RESULT 14 T34513 hypothetical C; Species: C. C; Date: 29-0 C; Accession:	~ ~ ~ ~ ~ ~
	OO EMVIEE		-
KATTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTP-RKMTSTMPELLNTSRIAE 1029	74 KATTPKPQKPTKA :    :	0	1 0
	844 ANSTPK	Db 84	п
-KTITTEIMNKPEETA-KPKDRATNS	920 TSTTTQDTTPFKITTLKTTTLAPKVTTTK-	Оу 92	Ю
TKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMIKETATTESTITESTITESTITESTITESTITESTITESTIT	60 TKTPAATKPEMTTTAKDKTTERDL :   :       : 88 SSDEDVSKAKKTNTAVSKSPV	Qy 86 Db 78	D Ø
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TAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPK 799 :::			y Qy
PAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTFKEFAFTTFNG /37		<b>.</b>	дy

RESULT T11622 extens: C;Spec: C;Date C;Arse: R;Arse: Rol. P A;Titl A;Titl A;Refe A;Stat A;Mole	Qу Дъ	Оу	Qy Db	Db Db	Qу	Qу	94 64	4d 40	Qу	QУ	Qy Db	Qу	ДУ	DP DV	do
1622 1622 Species: Classin classic classin classic classic classic classin classic cla	986 2890	931 2834	887 2774	836 2722	776 2668	723 2608	694 2548	648 2488	611 2432	561 2375	522 2316	470 2259	411 2204	352 2144	2086
RESULT 15  T11622 extensin class 1 precursor - cowpea C;Species: Vigna unguiculata (cowpea) C;Species: Vigna unguiculata (cowpea) C;Accession: T11622; S54155 R;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A. Mol. plant Microbe Interact. 10, 95-101, 1997 A;Title: Rhizobia modulate root-hair-specific expression of extensin genes. A;Reference number: Z17301; MUID:97155574 A;Accession: T11622 A;Accession: T1622 A;Molecule type: DNA	6 APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTT 1036	1 KITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDRATNSKATTPRPQKPTK 985 :	PETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTP-F 93	TPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTT 8     : :  :	KPAPTIPKETAPIIPKEPAPTIEKKPAPTIPETPPPITSEVSTPTITKEPITIHKSPDES 83	EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPT-STTSD 77  :     :     :      :      :   :   :	PTTTKEPTSTTSDKPAPTTPKGTAPTTPK-72	APTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA 69	TPEEPTTPEEPPKEP 647	PTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEEKPAPTTPEELAPT 610:	TTPKEPAPTTPKKPAPTTPKEPAPTTTKKPA 560	TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAP 521	N Q	PKEPAPTTTKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPK-EP 410	SPTEVHT-SSETK 21

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C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-489/Product: extensin class 1 #status predicted <MAT>
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A;Molecule type: mRNA
A;Residues: 326-489 <AR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-489 <ARS>
A;Cross·references: EMBL:x91836; NID:g1015936; PIDN:CAA62943.1; PID:g1015937
A;Experimental source: sub_species Red caloona
R;Arsen1jevic-Maksimovic, I: Broughton, W.J.; Krause, A.
submitted to the EMBL Data Library, April 1995
A;Description: A class of root-hair specific extensins involved in rhizobium/legume inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7
Best Local Similarity 31.2
Matches 149; Conservative
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               423
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                                                                                                                                                                                                             634 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA 693
                                                                                                                                                                                                                                                                          248
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SPP-----PPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPP 475
                                      KKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPP 811
                                                                              ----KSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSP 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 633; DB 2; Length 489; 31.2%; Pred. No. 6.8e-20; tive 33; Mismatches 252; Indels
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Search completed: April 26, 2002, 16:31:27 Job time: 682 sec

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Result
No.
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SLP1_CLOTM
Q06852;
01-JUN-1994
01-JUN-1994
01-FEB-1996
SEQUENCE FROM N.A.

STRAIN-NCIB 10682;

MEDLINE-93209931; PubMed-8458832;

MUDIOT., Beguin P., Aubert J.-P.;

"Organization of a Clostridium thermocellum gene cluster encoding cellulosomal scaffolding protein CipA and a protein possibly involin attachment of the cellulosome to the cell surface.";

J. Bacteriol. 175:1891-1899(1993).
                                                                                                                                                                                                                                                                                                                     OLPB.
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E GLYCOPROTEIN 1 PRECURSOR (OUTE
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-i- SUBCELLULAR LOCATION: CELL WALL.
-i- SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS.
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GLY/PRO/SER/THR-RICH.
SLH 1 (INCOMPLETE).
SLH 2.
SLH 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 950;
Pred. No. 4
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CELL SURFACE GLYCOPROTEIN

4 X 156 AA APPROXIMATE REI
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5F396695BA9FE74B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; I
1.5e-30;
hes 361;
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EPTPSDE
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AMYHLYEAT
ID AMYHLY 3
AMYHLYEAT
ID AMYHLY PO8640
AC P08640
DT 01-FBG
DT 20-AUG
DE GLUCOA
DE GLUCOA
DE GLUCOA
CS Saccha
OC Eukary
OC Saccha
OC STRAII
RN EGULE
RA GentLe
RA Rajann
RA Rajann
RA Rajann
RA Rajann
RA SEQUEN
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RA GentLe
RA Churc't
RA GentLe
RA Churc't
RA GentLe
RA GentLe
RA GentLe
RA FAJAN
RA SEQUEN
RA SEQUEN
RA FAJAN
RI [2]
RA YAMBASH
RI "Gene
RI J. BBAC
RN [3]
RN STRAII
RX MEDLII
RX FEBS :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AMYH_YEAST STANDARD; PRT; 1367 AA.
P08640; P08068;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAMYLASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
STA1 OR STA2 OR MAL5 OR YIR019C.
STA1 OR STA2 OR MAL5 OR YIR019C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1499
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Barrell B.G., Connor R., Copsey T., Dear S., Devlin K., Fraser

Churcher C.M., Connor R., Copsey T., Dear S., Jagels K., Jones

Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

walsh S.V., Whitehead S.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1601
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                     MEDLINE-89031230; PubMed-3141213; Pardo J.M., Ianez E., Zalacain M. "Similar short elements in the 5' from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                SEQUENCE OF 1-242 AND 762-1331 FROM N.A. MEDLINE-87194600; PubMed=3106330;
                                                                                                                                                                                         "Gene
                                                                                                                                                                                                              Yamashita I.,
                                                                                                                                                      Bacteriol. 169:2142-2149(1987)
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               E., Zalacain M., Claros ments in the 5' regions cerevisiae.";
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                                              M.G., J
of the
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                                                Jimenez A
e STA2 and
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Best Local S
Matches 328
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EMBL; M16154; AAA35014.1; -.
EMBL; M16165; AAA35015.1; -.
EMBL; X13857; CAA32069.1; -.
PIR; B26877; B26877.
PIR; A26877; B26877.
PIR; S48478; S48478.
SGD; S0001458; MUC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Multigene family.

SIGNAL 1 21

CHAIN 22 1367

DOMAIN 210 1367

CARBOHYD 817 817

CARBOHYD 874 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL 1,4-LINKED ALPHA-D-GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REDUCING ENDS OF THE CHWITH RELEASE OF BETA-D-GLUCOSE.
SIMILARITY: TO S.POMBE SPEC215.13.
SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKTKKVIESEEITEEHSVSENQESSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSTGCNNYDNQGHSQTDFPGFYWNIDCDNNCGGTKSSTTTSSTSES--STT---
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                                                                                                                                                                                                                         APTT----TKSAP----TTPKEPAPTTTKEPAPTTPKEPAP----TTTKEPAPTTTKSA
                                                                                                                                                                                                                                                                                                           PT--PSSSTTESSS-----APVPTPSSSTT-----ESSSAPVTSSTTESSS---
                                                                                                                                                                                                                                                                                                                                    PSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKDL
                                                                                                                                                                                                                                                                                                                                                                  PTTTSCTKEKPT - - PPHHD - - -
PKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT-TPEEPTPTTPEE
                                                                                                          APKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSA
                                                                                                                                       STTESSSAPVT----SSTTESSSAPV----PTPSSSTTESSSAPVT---SSTTESSSAPV
                                                                                                                                                                   PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP---TTPKEPAPTTKEPAPTTPKEPAPT
                                                                                                                                                                                               APVTSSTTESSSAPVTSSTTESSSAPVTSS----TTESSSAPVTSSTTESSSAPVPTPSS
                                                                                                                                                                                                                                                      APV----
                                                                                                                                                                                                                                                                               APTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEP
                             STTESSSTPVTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosidase;
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817
874
1367
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                                                                                    -PTPSSSTTESSSAPAPTPS
                                                                                                                                                                                                                                                     -PTPSSSTTESSSAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSS
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                              TTESSSAPVPTPSSSTTESSSAPVPT----PSSSTTESSSAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 809; DB Pred. No. 9.8e·12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCOAMYLASE S1/S2.
SER/THR-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MW; 91C00E2DBD61AA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                    -----TTPCT----KKKTTTSKTCTKKTTTPV
                                                          -TPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTA
                                                                                       SSTTESSSAPVTSS---TTESSSAPVPTPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degradation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                           ----APATPTTTSCTKEKPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1367;
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                                                                   TISSUE-Pancreas;
MEDLINE-90366716; PubMed-2394722;
Lan M.S., Batra S.K., Q1 W.-N., Metzgar R.S.,
"Cloning and sequencing of a human pancreatic
J. Biol. Chem. 265:15294-15299(1990).
   SEQUENCE FROM N.A.
MEDLINE=90202794; PubMed=2318825;
Ligtenberg M.J.L., Vos H.L., Gennis
"Episialin, a carcinoma-associated
                                                                                                                                                                                                                                                       MUCI_HUMAN STANDARD; PRT; 1255 AA.

P15941; P15942; P13931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;

O1-JAN-1990 (Rel. 13, Created)

O1-APR-1990 (Rel. 14, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEM)

(EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (ARCINOMA-ASSOCIATED MUCIN)

(TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEAR

REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN)
                                                                                                                                                                                            Eukaryota;
Mammalia;
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Primates;
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Catarrhini; Hominidae
    mucin,
   is
                                                                                                                                                                                       Hominidae;
 generated
                                                                                    Hollingsworth M.A.;
tumor mucin cDNA.";
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SEQUENCE FROM N.A.

MEDLINE=91033045; PubMed=1688329;
Tsarfaty I., Hareuveni M., Horev J., Zar
Jeltsch J.M., Garnier J.M., Lathe R., Ke
"Isolation and characterization of an ex
coding for a breast-cancer-associated ar
Gene 93:313-318(1990).
     Weiss M., Baruch A., Keydar I., Wreschner D.H.; "Preoperative diagnosis of thyroid papillary carcinoma transcriptase polymerase chain reaction of the MUC1 gen Int. J. Cancer 66:55-59(1996).
                                                                                                    MEDLINE-90088473;
Abe M., Siddiqui,
                                                                                                                                                                            SEQUENCE OF 1-169 FROM N.A
                                                                                                                                                                                                                                                   PARTIAL SEQUENCE FROM N.A.
MEDLINE-88330762; PubMed=3417635;
Gendler S.J., Taylor-Papadimitriou
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MEDLINE-90276413; PubMed=2351132;
MEDSINE-90276413; PubMed=2351132;
Wreschener D.H., Hareuveni M., Tsarfaty
Wreschener Paratsky J., Kotkes P., Weiss
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                                                             MEDLINE-96183746;
                                                                         FISSUE=Thyroid
                                                                                      SEQUENCE OF 1-109
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MEDLINE-90276414; PubMed-2112460;
Hareuveni M., Tsarfaty I., Zarets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      may generate multiple protein forms
Eur. J. Biochem. 189:463-473(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91097524; PubMed=2268309; MEDLINE=91097524; PubMed=2268309; Lancaster C.A., Peat N., Dublig T., Wils Taylor-Papadimitriou J., Gendler S.J.; "Structure and expression of the human gene: an expressed VNTR unit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Duhique Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D., Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.";
J. Biol. Chem. 265:15286-15293(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human epithelial tumor antigen cDNA
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TISSUE-Breast
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                                                                                                                                                                                                   immunogenic region of a huby carcinomas is made up o Chem. 263:12820-12823(1988)
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                                                         PubMed=8608966;
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.J.;
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EMBL; M61170; AAB53150 1
EMBL; X52229; CAA36477 8.1
EMBL; X52229; CAA36477 1
EMBL; M35023; AAB59612 1
EMBL; M35093; AAB59612 1
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EMBL; Z17324; CAA78973 .1
EMBL; Z17325; CAA78973 .1
EMBL; M31823; AAA35757 .1
EMBL; S81736; AAD14369 .1
EMBL; S81736; AAD14369 .1
EMBL; M21868; AAA59874 .1
PIR; B35175; B35175 .
PIR; B35175; B35175 .
PIR; B35175; B35175 .
PIR; S10218; S10218 .
GlyCoSuiteDB; P15941; -
GlyCoSuiteDB; P15941; -
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Yu C.J., Yang P.C., Shew J.Y., Hong T.M., Yang Lee L.N., Luh K.T., Wu C.W.;
"Mucin mRNA expression in lung adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buluwela L., Liu Q., Luqmani Y.A., Gomm J.J., Coombes R Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases -:- FUNCTION: DIRECT OR INDIRECT INTERACTION WITH ACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
TISSUE=Lung
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MIM; 113720;
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  CARBOHYD
CARBOHYD
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SMART; SM00200; SEA; 1.
PROSITE; PS50024; SEA;
                                                                                                                                                                                        Repeat; Alternative splicing SIGNAL 1 23
                                                                                                                                                                                                                               Glycoprotein;
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                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMORS, SUCH AS BREAST CANCER. PTM: HIGHLY GLYCOSYLATED (N-AND O-LINKED
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                                                                                                                                                                                                     hydroxyproline-containing decapeptide in the adhesive protein of the mussel, Mytlius edulis L.";

L. J. Blol. Chem. 258:2911-2915(1983).

C. -!- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSEL'S PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S PRODUCE ONE OF THERADS, CALLED A BYSSUS, FORMED BY A FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

C. -!- SUBCELLULAR LOCATION: SECRETED.

C. -!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

C. -!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

C. -!- DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEARS OF A DECAPEPTIDE.

C. -!- CTM: THE DECAPEPTIDE A-K-P-S-Y-P-T-Y-K IS POST-TRANSLATIONALLY MODIFIED AS FOLLOWING: THE SITTH AND SEVENTH RESIDUES ARE HYDROXYLATED AND THE PENULTIMATE IS A 3,4-DIHYDROXYPHENYLALANINE C. (DOPA) DERIVED FROM TYROSINE.
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                                   EMBL; X54422; CAA38294.1; -
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Q25460;
30-MAY-2000
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Mytiloidea; Mytilidae; Mytilus.
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLI
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                                                         s SWISS-PROT entry is copyright. It is produced through a collab-
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situtes requires a license agreement (See http://www.isb-sib.ch/an-
send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND POST-TRANSLATIONAL MODIFICATIONS PubMed=6298211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6:171-177(1990).
P_rich_extensn
                Adhesive_plaq.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
AKPTNPSTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAKP-
                       ALENSPK----EPGVPTT--KTPA-----ATKPEMTTTAKDKTTERDLRTTPETTTAAPK 895
                                                                     TTPKKPA-PTT----PETPPPTTSEVSTPTTTKE----PTTIHKSPDESTPELSAEPTPK
                                                                                                         TYKAKPSYPPTYKAKPSYKAKPTYPSTYKAKPSYPPTYKAKPSYP----PTYKAKPSYPP
                                                    TYKAKPTYPSTYKAKPSYPPTYKPKISYPPTYKAKPSYPPT-YKAKPSYPPTYKAKPTYK
                                                                                                                              TTLKEPA--PTTPKKPA--PKELAPTTTKG-PTSTTSDKPAPTTPKETAPTTPKEPA--P
                                                                                                                                                                      KTTYPPTYK----
                                                                                                                                                                                      KELAPTTIKEPTSTTSDKPAPTTPKGTAPTT----PKEPAPTTPKEPAPTTPKGT---AP
                                                                                                                                                                                                                                             PKEPAPTTPKEPAPTTPKE----PAPTTPKETAPTT--PKGTAPTTLKEPAPTTPKKPAP
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                                                                                                                                                                                                                                                                         YPST-YKAKPSYP----PSYKAKPSYPPTYKAKPTYKAKPT----YPSTYKA----K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTP 306
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PR01217; PRICHEXTENSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YPPTYKAKPSYPSSYKPKKTYPPTYK-----PKLTY----PPTYKP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KPKMTYPPTYKPKPSYPP-----TYKSKPTYKPK 104
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26.9%;
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Pred.
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No. 2
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.6e-15;
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ZAN_HUMAN
ZAN_HUMAN
ID ZAN E
AC Q9Y45
DT 20-AL
CO Mamman
RX MEDL:
RA G100!
RA TSU!
RT Trevel
RA TSU!
RT TRUE
RT TRUE
RT TOLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chromosome localization of the mouse zona zonadhesin gene (ZAN),"; Genomics 41:119-122(1997).
-i- FUNCTION: BINDS IN A SPECIES-SPECIFIC OF THE EGG. MAY BE INVOLVED IN GAMETE SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZAN_HUMAN STANDARD;
09Y493; 000218;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-2379 FROM N.A. MEDLINE=99018118; PubMed=9799793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2338-2700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reveals 17 genes.";
Genome Res. 8:1060-1073(1998).
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                                                  EMBL; AF053356; AAC78790.1; -. EMBL; U83191; AAC51208.1; -. MIM; 602372; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           849
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     InterPro;
                                 [nterPro;
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
SUBCELUILAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON SUBCELUILAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON SAPICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZONA PELLUCIDA.
                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
     IPR000998;
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                                 IPR000561;
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Pfam; PF00294; vwd; 4.
PFANTS; PR01217; PRCHEXTENSN.
SMART; SM00137; MAM; 2.
SMART; SM00011; VWC; 1.
SMART; SM00011; VWC; 61; 3.
SMART; SM00016; VWD; 3.
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EKPTISTEE--PTTPTEETTISTEKPSIPMEKPTLPTEETTTSVEETTISTEKLTIPM--
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IPR001007;
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IPR002919;
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                             CHAIN
                                                                                                                                                       EMBL;
                                                                                                                  Hydroxylation.
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-I- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. XANTHI; TISSUE-Leaf;
MEDLING-90118263; PubMed-2612909;
Keller B., Lamb C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P13983;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
01-MAR-1992 (Rel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOBAC
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HRGPNT3.
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PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED
                                                                                                                           ; X13885; CAA32090.1; S06733; S06733. at; Cell wall; Glycopi
                                                                                                                                                                                                                                                                               GLYCOSYLATED.
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                                                  EXTENSIN.
H-A-P-P.
H-A-P-P.
2 X 7 AA
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2.
CONTAINS THE SER-PRO(4)
3 X APPROXIMATE TANDEM I
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                                                                                                                          Signal;
                                                AA TANDEM
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                                                  REPEATS
  REPEATS.
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Best Local Sim
Matches 170;
    SEQUENCE FROM N.A.
MEDLINE-89121513; PubMed-3220257;
Julien J.-P., Cote F., Beaudet L.
Mushynski W.;
Sequence and structure of the mo
                                                                                                                     NIFH_MOUSE STANDARD: PRT; 1087 AA.
P19246; Q61959;
O1-NOV-1990 (Rel. 16, Created)
O1-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H).
                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                           NCBI_TaxID=10090;
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structure of the subunit.";
                                                                                    Chordata;
Rodentia;
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                                                                                Craniata; Vertebrata; ; Sciurognathi; Muridae;
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       mouse
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Pred. No. 4
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                        Sidky M., Flavell D.,
       gene
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      coding
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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  CONFLICT
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT
SUBSERVED BY THE TWO SMALLER NF PROTEINS.
SUBSERVED BY THE TWO SMALLER NF DEVELOS.
PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THE FORMATION OF
INTERPILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
OF AXONAL CALLBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEYELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT MITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

SIMILARITY: BELONG TO THE INTERMEDIATE FILAMENT FAMILY.

CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation burners Buropean Bioinformatics Institute. There are no restrictions on its European Bioinformatics as long as its content is in no way non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , M24496; AAA39813.1;
, M23349; AAA39813.1;
, M24494; AAA39813.1;
, M24495; AAA39813.1;
, M35131; AAA39809.1; A
, Z31012; CAA83229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68:307-314(1988)
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A43778; A4377
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  TISSUE-Brain;
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  COIL 2B.

K -> QA (IN REF. 2 AND 3).

A -> AR (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

P -> PREAKSP (IN REF. 3).

MISSING (IN REF. 3).

G -> A (IN REF. 3 AND 3).
                                                                                                                                                                                   LINKER 12.
COIL 2A.
LINKER 2.
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ROD.
TAIL.
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50 X 6 AA TANDEM
GLU/LYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKTKKVIESE--EITEEHSVS-ENQESSSSSSSSSSSTIWKIKSSKNSAANRELQKKLK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEPAPTTKEPAPTTPKEPA----PTAPKKP----APTTPKEPAPTTPKEPAPTTTKEPSP
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26.8%;
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pred. No. 6.4e
)6; Mismatches
                                                                          -KTTEDKATKGEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551; DB 1;
No. 6.4e-15;
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TCNA\_TRYCR P23253;

STANDARD;

PRT;

1162

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Query Match
Best Local S
Matches 177
                                                                                                                  DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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REPEAT
DOMAIN
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SEQUENCE FROM N.A.
STRAIN-SILVIO X-10/4;
MEDLINE-91277609; PubMed-1711561;
MEDLINE-91277609; Mejia J.S., Orteg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 01-NOV-1991 (Rel. 20-AUG-2001 (Rel. SIALIDASE (EC 3.2.)
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Trypom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91376547; PubMed=1896773;
Prioli R.P., Mejia J.S., Aji T.,
"Trypanosoma cruzi: localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fo its requires a license agreement (See http://www.isb-sib.send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               L; M61732; AAA30255.1;
JH0557; JH0557.
P29768; IDIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN EPIMASTIGOTES AND NO DETECTABLE IN AMASTIGOTES.
MISCELLANEOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE TNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO SIMILARITY: CONTAINS 3
                                                                                                                                                                                                                                                                                                                                                          PF0201
          Similarity 29., 77; Conservative
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                                                                                                                                                                                                                                                                                                                                   Glycosidase;
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20, Last sequence update)
40, Last annotation update)
.1.18) (NEURAMINIDASE) (NA)
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            100;
                                                                                            BNR 1.

BNR 2.

BNR 2.

BNR 3.

FIBRONECTIN TYPE-III.

44 X 12 AA TANDEM REPEATS, LTR DOMAIN

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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      Score 530.5;
Pred. No. 4.16
)0; Mismatches
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of neur
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  .5; DB 1;
4.1e-14;
ches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
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E
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                                                                                                                                                                                                                                                                                                                              GPI-anchor;
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                                        1162;
    113;
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  Proc. Natl. Acad. Sci. U.S.A. 90:11
[2]
SEQUENCE FROM N.A.
STRAIN=CANTON-S;
MEDLINE=93165730; PubMed=8434015;
Ballinger D.G., Xue N., Harshman K.
"A Drosophila photoreceptor cell-sp
calcium and contains a leucine zipp
                                                                                                                                                                           CPN OR CAP.
Drosophila me
Eukaryota; Me
Pterygota; Ne
Ephydroidea;
                                                                                                                                                                                                                                      CPN_DROME
Q02910;
Q1-OCT-1993
Q1-OCT-1993
Q1-FEB-1994
CALPHOTIN.
                                                                          MEDLINE-93165729; PubMed-8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                               SEQUENCE FROM N.A. STRAIN=CANTON-S;
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Metazoa; Arthropoda;
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Matches 233
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CONFLICT 36
CONFLICT 64
CONFLICT 76
CONFLICT 100
CONFLICT 126
CONFLICT 126
CONFLICT 154
CONFLICT 534
CONFLICT 703
CONFLICT 703
CONFLICT 721
SEQUENCE 865 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; L05080; AAA28420.1;
PIR; A47282; A47282.
                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 PKEPAPTTTKSAPTTP-KEPAPTTTKEPAPTTPKEPAPTTTKEPAPT----TTKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTIIKSAPTT
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SUBUNIT: HOMODIMER (PROBABLE).
SUBUNIT: HOMODIMER (PROBABLE).
SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT
FISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS
COMPOUND EYES AND OCELLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTIPAPAPIAAASVTPVASVAPPVVAAPTP----PAASPVSTPVAVAQIPVAVSAPVAP
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TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKE--
                                                            AAESIPAPVVATTPVPAT---LAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPP
                                                                                                         TPEKL-APTTPEKPAPTTPEELAPTTPEEPTPTTPEEP---APTTPKAAAPNTPKEPAPT
                                                                                                                                                     ETPALAPVVAESQVAANTVVATPPTPAPEPET IAPPVVAETPEVASVAVAETTPPVVPPV
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I -> T (IN REF 2)  
I -> V (IN REF 2)  
T -> A (IN REF 2)  
P -> AP (IN REF 2)  
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I -> V (IN REF 2)  
S -> T (IN REF 2)  
A -> E (IN REF 2)  
I -> T (IN REF 2)  
C -> T (IN REF 2)  
C -> E (IN REF 2)  
C -> T (IN REF 2
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T (IN REF. 2)
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30-MAY-2000
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Mytiloidea; Mytilida
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20-AUG-2001
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                                                                                                                                                                                                                                                                                            "Adhesive protein cDNA sequence of the mussel Mytilus coruscus and its evolutionary implications.";

J. Mol. Evol. 43:348-356(1996).

J. Mol. Evol. 43:348-356(1996).

FUNCTION: PROVIDES ADDESIVENESS TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSCLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A PIBROUS COLLAGENOUS CORE COAPTED WITH ADHESIVE PROTEINS.

FIBROUS COLLAGENOUS CORE COAPTED WITH ADHESIVE PROTEINS.

SUBCELLULAR LOCATION: SECRETED.

TYSSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND ALSO TYROSINE (THUS PRODUCING DOPA - 3,4-DIHYDROXYPHENYLALANINE)

ALSO TYROSINE (THUS PRODUCING DOPA - 3,4-DIHYDROXYPHENYLALANINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mytiloidea; Mytilidae;
NCBI_TaxID=42192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mytilus coruscus (Sea mussel).
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                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long
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PLAQUE MATRIX PROTEIN PRECURSOR (FOOT
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i Y., Takeyama S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 AKPTPKAETTTKGPALTTPKEPT-PTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTK 346
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PRINTS; PR01216; ADHESIVEI
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
ISYPSTYKAKP----SYPPTYKPKPSYASSYKPKIRYPPTYKPKPSYASSYK-----PK 785
                       RTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPK 943
                                               Y---PPSYKPKKTYPPTYK-----PKISYPPTYK----TKPSYPASYKRKTSYPPTYKPK 735
                                                                 IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT----TERDL 883
                                                                                                 PPTYKPKITYPPTYK-PKPSYPPSYRPKITYPPTYKPKKSYPQAYKSKGSYPPSYQPKKT
                                                                                                                                                ------PKITYPPTYK-PKPSYPTPYKOKPSYPPIYKSKSSYPTAYKSKKTY 628
                                                                                                                       PTT--PKETAPTTPKEPAPTTPK--KPAPTTPET-----PPPTTSEVSTPTTTKEPTT
                                                                                                                                                                        EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP----KKPAPKELAPTTTKGPTSTTSDKPA 778
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                                                                                                                                                                                                                                                PTYKPKPSYPPTYKPKITYPPTYKRKPSYPTPYKQKPSYPPIYKSKSSYPTSYKSKKTYP
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ADHESIVE LAQUE MATRIX PROTEIN.
NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-[IP]-[ST]-Y-P-[PST].
NONAPETIDE 1.
NONAPETIDE 2.
MW; 98CC70D7C75FF3C4 CRC64;
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EING ALTERED DEVELOPMENTALLY AT THE NEUROPILAMENT FUNCTION. INTERMEDIATE FILAMENT FAMILY. FERS FROM THAT SHOWN FROM POSIT A FRAMESHIFT.	HOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE 1 LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AN	SERINES IN THIS MOTIF. IT IS H RESULTS IN THE FORMATION OF RE IMPORTANT IN THE MAINTENANCE	E 13	FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTI	U.S.A. 86:2463-2467/1989	COLING THE PART HIGH MOLECULAR Weight (NF-H): developmental and tissue expres	S., Anderson J., B.S., Breitner J	Med=2928342;	209:203-205(1	on of a cDNA for the rat h	; PubMed=2878828; ion D., Anderton B.H	D 243-313 FROM N.A.	лимин. 154:1099-1106(1988).	"The large neurofilament subunit (NF-H) of the rat: cDNA cloning and	Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L., Jolles P.:	NCE OF 37-831 FROM N.A.	8(1988).	ial sequence of the rat heavy neurofil	K.C., Robinson P.A., Wion D., Anderton B u	SEQUENCE FROM N.A. TISSUE-Brain;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		OLYP	Last annotation update)	<ol> <li>15, Created)</li> <li>28, Last sequence :</li> </ol>	NFH_RAT STANDARD; PRT; 831 AA. P16884; Q63368;	SULT 12 H_RAT	828 YPPTYKPKISYPPTYKPKITYPPTYKPKISYPPAYKPKISYPSQ 871		RYPPTYKPKPSYASSYKPKIT	944 VTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKP-TSTKKPK-T 998

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Pfam; PF00038;
PROSITE; PS0022
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EMBL;
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SL; X13804; CAA32038.1; A

SL; M21964; AAA41695.1;

SL; J04517; AAA41692.1;

AAA41692.1;

AAA41692.1;

AAA4469; AAA44692.1;

AAA4469; AAA44692.1;

AAA4469; AAA44692.1;

AAA4469; AAA44692.1;

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AAA4469; AAA4693.1;

AAA469; AAA4693.1;

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AAA4693; AAA4693; AAA4693.1;

AAA4693; A
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                                                                                                        PKEPA----PTTTKEPA----PTTTKSAPTTPKEPA----PTTPKKPA----
                                                                                                                                                                             KSPAEVKSPAVAKSPAEVKSPAEVKSPAEAKS-PAEAKSPAEVKSPATVKSPGEAKSPAE
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                                                                                                                                                                                                                                                                                                                              VKSEEKIKVVE-
                                    EVKSPVTVKSPAEAKSPVEVKSPA-SVKSPSEAKSPAGAKSPAEAKSPVVAKSPAEA--K
EPAPTTPKEPAPTTTKEPSPTTPKEPA----PTTTKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001664; IF.
                                                                  -PTTPKEP----PTTPKEPAPTTKEP----APTTPKEPA----PTAPKKPAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276
1164
1193
1193
1193
346
373
482
482
570
591
727
759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- DNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641
164
185
193
193
346
373
482
485
571
591
727
759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; U-
26.6%; Pred
76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89486
                                                                                                                                                                                                                                                                                                                              -----KSEKETVIVEEQTEEIQVTEEVTEEEDKEAQGEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 517.5; DB 1;
Pred. No. 9.8e-14;
76; Mismatches 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP - R ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L -> I (IN REF. 2).
L -> S (IN REF. 2).
L -> T (IN REF. 2).
M -> T (IN REF. 2).
M -> T (IN REF. 2).
K -> N (IN REF. 1).
A -> V (IN REF. 1 AND 4).
G -> E (IN REF. 2 AND 4).
P -> S (IN REF. 2).
R -> V (IN REF. 2 AND 4).
A -> V (IN REF. 2 AND 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
T -> L (IN REF. 2 AND 4).
R -> P (IN REF. 2 AND 4).
1B0973C3F13EF768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil; Neurone; Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AA TANDEM REPEATS OF K-S-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
       -APTTKEPAPTTKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179;
                                                                                                                                                  PTTPKEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                      264
                                                                                455
                                                                                                                    421
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                                                                                                                                                                                        362
                                                                                                                                                                                                                                                               303
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           503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
1NTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hauser F., Hoffmann W.;
"P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic polymorphism.";
J. Biol. Chem. 267:24620-24624(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q05049;
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790
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                                                                                                                                                                                 or send an
                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - ! - SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: A NUMBER OF DIFFERENT MAY BE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: SKIN. PTM: EXTENSIVELY O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVEEEKTPATPKTEVKESKKDEAPKEAOKP-KAEEKEPLTEKPKDSPGEAKKEEA----K 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFECTIONS. PROTECTS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KGLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPED
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                                                                                                                                                                                   equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                    institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE EPITHELIA FROM SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
esobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EKTTESKKREEKPKMEAKAKEED-----
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                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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Pfam;

InterPro; IPR000519; P\_trefoil
Pfam; PF00088; trefoil; 6.

PF00088; trefoil;

PIR; A45155; A45155. HSSP; P04002; 1WFA. EMBL; L02115; AAA74725.1;

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В
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                                                                                             Query Match 7.0%; Score 509.5; DB 1; Best Local Similarity 28.1%; Pred. No. 1.6e-13; Matches 223; Conservative 48; Mismatches 276;
                                                                                                                                                                                                                                REPEAT
DISULFID
DISUL
                               250 TINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEP 309
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Repeat; A
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DOMAIN
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TTAAAVAATGKDTTAAAEGSAAAEKTAA-----AGEVSAPPT--AAVAATGEDATT----
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                                                                                                                                                                                                                           415 T
67774 MW;
                                                                                                                                                                                                                                                                               P_TREFOIL; 6.
skin; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                 3-1.
3-2.
3-3.
3-4.
3-5.
3-6.
3-7.
3-10.
3-10.
3-11.
3-12.
P-TYPE 4.
P-TYPE 5.
P-TYPE 6.
P-TYPE 5.
P-TYPE 6.
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P-TYPE 
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P-TYPE 1.
8 x APPROXIMATE TANDEM REPEATS, THR-RICH.
2-1.
2-2.
2-3.
2-4.
2-5.
2-6.
2-7.
2-8.
2-8.
P-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 X 8 AA APPROXIMATE TANDEM REPEATS, ALA/THR-RICH.
1-1.
1-2.
1-3.
1-4.
1-5.
1-6.
                                                                                       Indels 247; Gaps
                                                                                                                                              Length 662;
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                                                                                             30;
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ULT 14  IL-HUMAN  RPBI_HUMAN  RPBI_HUMAN  RPBI_HUMAN  RPBI_HUMAN  STANDARD;  PRT; 1970 AA.  P24928;  01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1). POLR2A,  HOMO Sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  CBL_TaxID-9606;  SEQUENCE FROM N.A.  MEDLINE-92178992; PubMed-1542581; Wintzerith M., Acker J., Vicaire S., Vigneron M., Kedinger C.;  "Complete sequence of the human RNA polymerase II largest subunit.";  Nucleic Acids Res. 20:910-910(1992).	TPKEPAPTTIKSAPTTTKEPAPTTKEPAPTTKEPAPTTPKEPAPTTP	310 TPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTAAAGAPTTAAAGAPTTTAAAGAPTTTAAAGAPTTTAAAGAPTTTAAAGAPTTTAAAGAPTTTTAPATTAAAGAPTTTAKEPAPTTTKEPAPTTPKEPA- 42

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Matches 181
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pfam; pF00633; RNA_pOL_A2; 1.

pfam; pF01854; RNA_pOL_A2; 1.

prosite; pS00115; RNA_POL_II_REPEAT; 43.

pRosite; pS00115; RNA_POL_II_REPEAT
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EMBL; X74874; CAA52862.1; JOINED.
EMBL; X74873; CAA52862.1; JOINED.
EMBL; X74872; CAA52862.1; JOINED.
EMBL; X74871; CAA52862.1; JOINED.
EMBL; X74870; CAA52862.1; JOINED.
PIR; S21054; S21054.
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                            363
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                                                                   481
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SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATE PTM: THE PHOSPHORYLATION ACTIVATES POL2.

THE PHOSPHORYLATION ACTIVATES POL2.

MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RIBO
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CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180660; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
                                                                                                                                                                                                                                                                        PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP--APTTPKEPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPTTPKEPASTTPKE-PTPTTIKSAPTTPKEPAPTTTKSAPTTPKE-----PAPTTTKE 362
                                                                PAPTTTKSAPTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTP
                                                                                                                                                                                  PSPMGGISPAMTPWNQGATPAYGAWSPSVGSGMTPGAAGFSPSAASDASGFSPGYSPAWS
-SPTSPSYSPTSPSY-SPTSPSYSPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSP
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IPR000722; RNA_pol_A.
IPR002879; RNA_pol_A2.
0623; RNA_pol_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 503.5; DB 1;
Pred. No. 6.9e-13;
Pred. No. 6.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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                                                                                                                                                                                                                                                                                       RA Lees J.F., Shneidman P.S., Skuntz S.F., Carden M.J., Lazzarini R.A.;

"The structure and organization of the human heavy neurofilament
subunit (NF-H) and the gene encoding it.";

EMBO J. 7:1947-1955(1988).

C. -i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT
CSUBSERVED BY THE TWO SMALLER NF PROTEINS.
CC --i- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS
CHORGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
OF AXONAL CALIBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFH_HUMAN
P12036;
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01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROPILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEFH OR NFH.
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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 X15306;
X15307;
X15308;
X15309;
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                                  CAA33366.1;
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Primates;
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Best Local Similarity 26.7
Matches 209; Conservative
794 APTTPKKPAPTTPETPPPTTSEV--STPTTTKEPTTIHKSPDE---STPELSAEPTPKAL 848
                                                                                       853 TEEKKDSKKEEAPKKEAP----KPKVEEKKEPAVEKPKESKVEAKKEEAEDKKKVP---T 905
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                                                                                                                                                                                          741 - KEEAKSPEKAKSPEKAKTLDVKSPEAKTPAKEEARSPADKFPEKAKSPVKEEVKSPEKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 VSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKE-KT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 KKTKKVIESE--EITEEHSVS-ENQESSSSSSSSSSTIWKIKSSKNSAANRELQKKLK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 VKMALDIEIAAYRKLLEGEECRIGFGPIP------FSLPEGLPKI--PSVST--HIK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 VK------DNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 KSTKDSLERQRSELEDRHQADIASYQEAIQQLDAELRNTKWEM-----AAQLREYQDLLN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001664; IF. Pfam; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intermediate filament;
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MIM; 162230; -.
                                                          PRGTAP--TTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPA-PTTPKETAPTTPKEP 793
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                                                                                                       KEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTT 736
                                                                                                                                         KSPLKADAKAPEKEIPKKEEVKSPVKEEEKPQEVKVKEPPKKAEEEKAPATPK-----
                                                                                                                                                                EEPAPTTPKAAAPNTPKEPAPTTP----KEPAPTTPKEPAPTTPKETAPTTPKGTAPTTL 676
                                                                                                                                                                                                                                                                APTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTA 563
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PS00226; IF; 1.
Neurone; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356; Indels 136;
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Db 958 KEEKAKK-----PEEKPKTEAKAKEDDKTLSKEPSKPKAEKAEKSSSTDQKDSKPPEKAT 1012

Qy 849 EN 850
| :
| Db 1013 ED 1014
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Search completed: April 26, 2002, 16:32:21 Job time: 571 sec

Sequence

55, Appl
126, Appl
27, Appl
27, Appl
28, Appl
36, Appl
37, Appl
37, Appl
38, Appl
38, Appl
38, Appl
314, Appl
326, Appl
328, Appl
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                              Issued_Patents_AA: *
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/cgn2_6/ptodata/2/laa/B_COMB.pep:*
/cgn2_6/ptodata/2/laa/Backfiles1.pep:*
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US-09-041-886-23
US-09-043-116-5
US-09-083-116-2
US-09-083-116-2
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US-08-642-255-132
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US-08-642-255-101
US-08-177-255-101
US-08-177-27A-75
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US-08-397-633A-50
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US-08-700-651-5

US-09-103-429A-3

US-08-928-361B-6

US-07-638-431-2

PCT-US92-00018-2

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US-08-928-361B-5
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501.094 Million cell updates/sec
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Sequence 5, Appli
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Sequence 132, Appl
Sequence 132, Appl
Sequence 137, Appl
Sequence 103, Appl
Sequence 20, Appli
Sequence 103, Appl
Sequence 104, Appli
Sequence 105, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
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                                                                       OPERATING SYSTEM: PC-DOS/MS-UUS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,429A
FILLING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORREY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: 351-39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
TELEFAX: (607) 256-2000
TELEFAX: (607) 256-300
TELEFAX: (507) 256-300
TELEFAX: 1007
T
                                                                               US-09-103-429A-4
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US-09-103-429A-4
     Query Match
Best Local Similarity
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CITY: Ithaca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09103429A Patent No. 6187558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: cDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
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Pred.
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US-08-478-029A-65
US-08-472-255-126
US-08-397-633A-26
US-08-395-267A-2
US-08-325-267A-2
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US-08-325-267A-6
US-08-325-257-10-61A-6
US-08-70-19-849-6
US-08-70-219-849-6
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US-08-642-255-114
US-08-642-255-114
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US-08-320-559-28
US-08-320-559-28
US-08-320-559-26
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522; DB 4;
No. 9.2e-26;
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Result

Length 805;

Database

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               GENERAL INFORMATION:
APPLICANT: Petersen, Ca
TITLE OF INVENTION: PEP
TITLE OF INVENTION: THE
TITLE OF INVENTION: SPE
TITLE OF INVENTION: SPE
TITLE OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                     Sequence 5, Application US/08928361B Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
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          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEPAPTT - - -
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                                                                                                                                                                                                                     ELSAEPTPKALENSPKEPGVPTTKTPAATKPE 869
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                                                                                                                                                                                                                                                            APTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPITIHKSPDESTP
                                                                                                                                                                                                                                                                                             TTAVPEIPTT-----VTSPPTAAPTT-AAPAPNT-----
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          PETERS, VERNY,
Sherman
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                                    SPECIES INFECTIONS 30
                                                            CATCOLYN
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
PEPTIDES, POLYPEPTIDES, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TKSAPTTPKEPAPTTKEPAPTTPKEPAPTTTKEPAPTTTK 385
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le, Suite
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  BIKSA
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Best Local Similarity
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STATE:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                     TESE--EITEEHSVSENQESSSSSSSSSSSSTIWKIKSSKNSAANRELQKKLKVKDNKKN 165
                                                                                                                                                                                                                                                                     ENPYTGNLVSRSTGKTIPNTYAGVYRSNETKTTEPSANTNFLLVDPKINAPCNSENSFEQ
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                                                                                                                                                                                                                                                                                                                       GWKQ---
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                      KKPTTTTATTTTTSETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFT
                                              KEPSPTTTKEPAPTTPKEPAPTTPKK----
                                                                                          PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTP
                                                                                                                       TTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKK 448
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539;

Indels 470;

49;

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328 286 268

341

455

508 509 534

569

395

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COMPUTER READALE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IEM PC compatible
COMPITERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA;
APPLICATION UMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                           TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1837 amino acids
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         NAME: Verny, Hana
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                         650-324-1678
                                                                                                                                                                                                                                                                                                                                                   UMBER: US 60/026,062
13-SEP-1996
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Score 513; DB 3; Pred. No. 9.2e-25;
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                     Length 1837;
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RESULT 3
5202236-25
; Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
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                                                                                                                                                                                                                                                                                                                                                                            GIVSGKRGLPPIEDENGNLFDPSTKLPIDGNNQLVNPETNSTVSGSTSGSTKPKPGIPVN
                                                                                                                                                                                                                                                                                      AEGETPHMLLRPHVEMPEVTPD-----MDYLPRVPNQGIINP------
                                                                                                                                                                                                                                                                                                                  GGGVVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNI----INP--ETGKV 1297
                                                                                                                                                                                                                                                                                                                                       TTTQVTSTTTQDTTPFKITTLKTTTLAPK--VTTTKKTTTTTEIMNKPEETAKPKDRAT-
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APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
SEQ ID NO:25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.0%; Score 506.5; DB 6; Best Local Similarity 29.9%; Pred. No. 8.2e-25; Matches 239; Conservative 78; Mismatches 308;
    720
                                   868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKE 268
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                           KETATTTEKTTESKITATTT
YKAKPTYPSTYKAKPTYPST
                                                     PSYP--PTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAKPSYPPTHKAKPT
                                                                                                               YKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAK
                                                                                PKEPGVPTTKTPAA-----TKPEMTTTAKDKTTERDLRTTPETTTAAP-----KMT
                                                                                                                                         ---TPETPPPTTSEVSTPTTTKE----PTTIHKSPD----ESTPELSAEPT-PKALENS
                                                                                                                                                                                            -PTTPKKPAPKELAPTTTKGPT--STTSDKPAPTTPKETAPTTPKEPAPTTPKKPA--PT
                                                                                                                                                                        PPTYKAKPTYK-AKPTYKAKPTYPSTYKAKPSYSPTYKAKPSYP----PTYKAKPSYPPT
                                                                                                                                                                                                                                     SYPPTYKAKPTYPSTYKAKPTYK--ARPSYP----PTYKAKPS-----YPPTYKAKPSY 546
                                                                                                                                                                                                                                                             ELAPTITKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPA- 749
                                                                                                                                                                                                                                                                                                 SYPPTYKPKISYPPTYKAKPSYPSTYKAKSSYPPTYKAKPSYPSTYKAKSSYPPTYKAKP
                                                                                                                                                                                                                                                                                                                     KEPAPTTPKEPAPTT----PKEPAPTTPKETAPTT--PKGTAPTTLKEPAPTTPKKPAPK 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A--PTTPKEPA--PTTPKEPA--PTTTKKPA--PTAPKEPAPTTPKETAPTTPKKLTPTT : || || || :| : || || || :| :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPA---PTTPKEPA----PTTPKKP 535
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                                                                                                                                                                                                                                                                                                                                                                                                                         SYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKVKPTYKAKPTYPS
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RESULT 4 US-08-700-651-5

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: WELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: STITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORIGHUM PARVUM
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORIGHUM PARVUM
TITLE OF INVENTION: NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 08/08/700,651B
COURSENT A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 --SKNSAANRELOKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQ 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 SITSGERKDPNKQAT-------ISGSRSCGWKQGYSIDSSTGFRVDSITGLPT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 STTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSTIWKIKS----- 143
                                                                                                                                                                                                                                                              438 VIGKDGRIENGMAFTMIPNDDTHVRFRFKVKDVGNTISVRCRKGAGKLEFPDRSLDFTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300;
                                                    AIHSGYQTSADFVTTTTAKPTTTT--TGAPGQPTTTTTGSPSKPTTTTTTKATTTT---- 607
                                                                                                ---PAPTTPKEPAPTITKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKP 599
                                                                                                                                                           PVAGHNSCSIIVGVSGDGKIHVSPYGSKDVSLIS----APIQPSELFNEVYCDTCTAKYG 553
                                                                                                                                                                                                                                                                                                                                                                     TKPTTTTTTTTTKKPTTTTTATTTTTSETESVIKPDEWCWLEKNGECEAKGATYVG
  APTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTT 659
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                                                                                                                                                                                                             -----APTTPKEPAPTTPKKPAPTTPKE----
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21.8%; Pred. No. 6.2e-24;
vative 94; Mismatches 510; Indels 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08700651B
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COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTA RELEASE #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/103,429A
FILING DATE: 24-JUN-1998

Version

#1.30

FILING DATE:

ZIP: 14850

COUNTRY:

NY USA

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, pinnisi & Michaels, P.C. STREET: 118 No. 6187558th Tioga

STREET: 118 | CITY: Ithaca

CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:

TELEFAX: (607) 256-3628
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acids

HYPOTHETICAL: N

MOLECULE TYPE:

TOPOLOGY:

linear . protein

LENGTH: 786 amino acids
TYPE: amino acid
STRANDEDNESS: single

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Trichoplusia ni
; TISSUE TYPE: peritrophic membrane
US-09-103-429A-3
                                                                                                                                                                                  655 PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPK 714
                                                                                                                                                                                                                     534 --PAPTAAPTAAPTTAAPESPTTVTVP-PTAAPTAAPTTAVPEIPITVT---SAPTAAPT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 DGEISPAPPVTEGNEDEDIDIGDLLDNGCPANFEIDWLLPHGNRCDKYYQCVHGNLVERR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ELLPNGCPADFDIHLLIPHDKYCNLFYQCSNGYTFEQRCPEGLYFNPYVQRCDSPANVEC
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REFERENCE/DOCKET NUMBER: BTI-39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
                                         DKPAPTTPKETAPTTPKEPAPTTPKKP 801
                                                                             TAAPTT-AAPAPNTTVTVPPTAAPTAAPPTVAH----
                                                                                                          GTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS 774
                                                                                                                                                    AAPTAAPTAAPTTAVPEIPTTVTSPPTAAPTTAAP---APNTT
                                                                                                                                                                                                                                                         EKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNT--PKEPAPTTPKEPAPTTPKE 654
                                                                                                                                                                                                                                                                                               NQCTSTAAPTAAPTAAPTAAPTA---APSTVVPPATPPATAAPVPPTT---AIPT--
                                                                                                                                                                                                                                                                                                                                                                                                          APTT----PKEP-------APTTPKKPAPTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGTHFSFELQQCDHIELVGCTLPGGESEEVDVDEDA-CTGWYCPTEPIEWEPLPNGCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EPAPTTT--------
                                                                                                                                                                                                                                                                                                                                ---PKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTP 596
                                                                                                                                                                                                                                                                                                                                                                      ADFSIDHLLPHESDCGQYLQCVHGQTIARPCPGNLHFSPATQSCESPVTAGCQVFECDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTQ--APTTTQ--ATTT---QAPTTTTQ-APTTTTQAPTTTTQ-APTTTQ--APTTTQ- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%; Score 498.5;
29.1%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEP
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                                                                                                                                                  ------VTVPP 632
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60, FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION: NAME: Verny, Hana
REGISTRATION NUMBER: 30,51
REFERENCE/DOCKET NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
             212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1721 amino acids
                               299 KGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT
                                                                                     190
                                                                                                                                            130 YAGVYRSNETKTTEPSANTNELLVDPKINAPCNSENSFEQGQIFDMGSKVYIPYTKCVGV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                              202 HNKVSTSPKITTAKP------INPRPSLPPNSDTSKE-----TSLTVN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                       144 --SKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQ 201
                                                                                                                                                                                                                    84 DPYSNCPFN-----PVTGNLVSRSTGKTIPN----TYAGVYRSN-ETKTTEPSANT-- 129
                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                               90 STTKRSPKPPNKKKTKKVIESEETTEEHSVSENQESSSSSSSSSSSSTIWKIKS-----
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STREET: J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 12-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
KETTVETKETTITNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTT 298
                                                                                                                                                                                                                                                                                           300;
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                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 498.5; DB 3; ilarity 21.8%; Pred. No. 7.2e-24; Conservative 94; Mismatches 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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13-SEP-1996
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Query Match Best Local Similarity Matches 200; Conserv

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKE-------
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                                                                                          VEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD------MDYLPRVPNQGIIINP--
                                                                                                                          GTTKPKPGIPVNGGGVVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNI--
                                                                                                                                                                                                                                                      INPTNNNTMDSSFAGAYKYAVSNGIKTDNVYGLPVGEITGLPKDPGSDIPFNSTTGELVD 1054
                                                                                                                                                                                                                                                                                   TTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP--EETAKPKD-----RATNSKATT
                                                                                                                                                                                                                                                                                                                   LMYDIESGRLIGQVSKRPIPGSIAGDLNPIMKTPTQTDSVTGKPIDPTTGLPFNPPTGHL
                                                                                                                                                                                                                                                                                                                                                                                 FSPEIEDGGIIPPEVAAANADKFKLSIP--PSVP-----ESIPE-----KDQKIDSISE
                                                                                                                                                                                       PSTGKPINNSTAGIVSGKPGLPPIEDENGNLFDPSTNLPIDGNNQLVNPETNSTVSGSTS
                                                                                                                                                                                                                      PKPQKPTKAPKKPTSTKKPKTMP--------RVRKPKTTPTPRKMTS
KLPIPGSVAGDEILTEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNGTLV
                                                            --INP--ETGKVIPGSLPGSLNYPSFNTPQQTDETTGKPVDTVTGLPYDPSTGEIIDPAT
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                                 -DLRTTPETTTAAPKMTKETATTTEKTTESKITATT-TQVTSTTTQD
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                                   ---PVDGLTTLRNGTLV 1122
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RESULT 7
US-07-638-431-2
; Sequence 2, Application US/07638431
; Patent No. 5198535
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEPAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
TRODOTORY: 1:coar
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Best Local Similarity
Matches 153; Conserv
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APPLICANT: Hoffman
APPLICANT: Charoe
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APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria
TITLE OF INVENTION: immunogen and dama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: A. David Spevack
STREET: NMRDC Building 1 T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, Avrom D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,
FILING DATE: 19910110
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
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STREET: Medica
CITY: Bethesda
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                                                                                                                         PNKPNP----NEPSNPNKPNPN-----EPLNPNEPSNPNEPSNPNAPSNPNE--PSNPNE
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SNPNE - - PLNPNEP - - -
                           TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 668
                                                                                         PAPTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP 609
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Charoenvit, Yupin
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                              NPNEPSNPNEPSNPNE -- PSNPKK---
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   --SNPNEPSNPNEPSNPEE---PSNPKE---PSNPNE---
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                                                                                                                                                                                                                                                                                                                                                                                          Score 488.5; DB 1;
Pred. No. 1.3e-23;
4; Mismatches 223;
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NAME: Spevack, Avram D.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
MOLECULE TYPE: protein
PCT-US92-00018-2
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Best Local Similarity 26.4
Matches 153; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20814-5044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00018
FILING DATE: 19920103
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATIN:
NAME: SCRUET INFORMATIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9200018
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
435 PTTPKEPAPTAPK--KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTT 492
                                      379 PAPTITKSAPTTPKEP-APTTPKKP-APTTPKEP-APTTPKEP-TPTTPKEPAPTTKEPA 434
                                                                                                              273 TPCKVRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNNPNN 332
                                                                                                                                      326 TPTTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEP----APTTPKEP-APTTTKE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
TITLE OF INVENTION: immunogen and gene encoding
NUMBER OF SPEQUENCES: 2
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ADDRESSEE: A. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: NMRDC Building 1 T-12 National Naval STREET: Medical Center CITY: Bethesda STATE: MD
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26.4%; Prec
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                                                                                                                                                                                          Score 488.5; DB 5;
Pred. No. 1.3e-23;
4; Mismatches 223;
                                                                                                                                                                                    Indels 149; Gaps
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4	TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKE 32.	. 269 T	Db	
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45;	Match 6.5%; Score 476.5; DB 6; Length 652; Local Similarity 29.7%; Pred. No. 5.7e-23; es 221; Conservative 71; Mismatches 284; Indels 169; Gaps	Mat	Z BO	
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                                                                                  ; OTHER INFORMATION: ; OTHER INFORMATION: US-09-219-849-5
                                                                                                                                                                                             SOFTWARE: Pa
SEQ ID NO 5
LENGTH: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09219849 Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                    APPLICANT: WERTEN, MARC W.T.

APPLICANT: WIND, RICHELE D.

APPLICANT: VAN DEN BOSCH, TANJA J.

TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF

FILE REFERENCE: 2728-2

FILE REFERENCE: 2728-2
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
 Matches 173;
                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                TYPE: PRT
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                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYP----PTYKAKPSYPPTYKVKPT--YK
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VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
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 Conservative
                                                                                                           Description amino acid :
6.2%; Score 452; DB 4; 1
25.6%; Pred. No. 3.3e-21;
tive 60; Mismatches 309;
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                                        Length 960;
         Indels 134;
           Gaps
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                                                                                              801 PAPTTP----ETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALEN-----S 851
                                                                                                                              581 GP--PGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGP--PGA 636
                                852 PKEPGVPTTKTPAATK
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 SRDPGPPGAHGPAGPK
                                                                PGPAGPPGSRDPGPPGAPGPAGPPGSRDPGP-PGAPGPAGPPGSRDPGPPGAPGPAGPPG 695
                                                                                                                                                              APTTPKKPAP-----KELAPTTTKGPTST--TSDKPAPTTPKETAPTTPKEPAPTTPKK 800
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RESULT 11
US-09-041-886-23
US-09-041-886-23
Sequence 23, Application US/09041886
Sequence 23, Application US/09041886 TITLE OF INVENTION: Proapoptotic TITLE OF INVENTION: Polypeptides NUMBER OF SEQUENCES: 72 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: APPLICANT: Bredesen, APPLICANT: Rabizadeh, CURRENT APPLICATION DATA: STREET: CITY: S COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, COUNTRY: STATE: APPLICATION NUMBER: ADDRESSEE: 92122 San Diego California E: Campbell & Flores LLP 4370 La Jolla Village Dr United States Bredesen, Dale E. Sharroz US/09/041,886 Drive, Peptides, Dependence and Methods of Use Version Suite #\_

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FILING DATE:
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91.915
REFERENCE/DOKET NUMBER: P-LJ 26
FELECOMMUNICATION INFORMATION:
FELEPHONE: (619) 535-9901
TELEFAX: (619) 535-9901
TELEFAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
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619 SPAGYKTASPPGPPPYGKRAPSPGAYKTATPPGYKPGSP-----PSFRTGTPPGYRG---
                                  712 TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTS 771
                                                                                                                    655
                                                                                                                                      501 NSGPPPPGAFPHPLEGGSSHHAHPYAMSPSLGSLRPYPPGPAHLPPPHSQVSYSQAGPNG
                                                                                                                                                                                                     441 GPPPPPPYGRLLANSNAHPGPFPPSTGAQSTAHPPYSTHHHHHQQQQQQQQQQQQQQQQHHG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 KEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPT 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 KNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 SMSMRSGRKKEAPGPR------EELRSRGRASPGGVSTSSSDG------KAEKS 50
                                                                                         PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKDAPKELAP---TTTKEPTSTTSDKPAPT 711
                                                                    PPVSSSSNSSSSTSQGSYPCS--HPSPSQGPQGAPYPFPPVPTVTTSSATLSTVIATVAS
                                                                                                                                                                     --TPEEPAP-----APTTPKAAAPN----TPKEPAPTTPKEP-----APTTPKE 654
                                                                                                                                                                                                                                                                     SSSSASPFPAS--QALPSYPHSFPPPTSL----SVSNQP----PKYTQPSLPSQAVWSQ 440
                                                                                                                                                                                                                                                                                                                                           MGQGMGGLPPGP---EKGPTLAPSPHSLPPASSSAPAPPMRFPYSSSSSSSAAASSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                          GGGNLPSAPPPANFPHVTPNLPPPPALRPLNNASASP----PGLGAQPLPGHL--PSPYA
                                                                                                                                                                                                                                                                                                       PTTPKKPAPTTPKEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLT--- 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| :
ROPEASF------EPHPSVTPTGYHAPMEP-PTSRMFQAP--PGAPPPHPQLYPGGT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKETOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTP--KEPASTTP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETNAPKKTKTEQELPRPQSPSDLDSLDGRSL--NDDGSSDPRDIDQDNRSTS-----P 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQTA------KKARVEEASTPK---VNKQGRS------EEISESESE 82
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     670
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PF P	0 0 0	SUI Seq -08	04 04 04 04	Db VQ	DB 04 DB 04	Db CS
CLA APP FIL AIOR APP FIL AIOR APP FIL IOR APP FIL FIL FIL FIL TORN NAME REGI	CORRESPONDENCE ADDRESSEE: STREET: P.O CITY: Alexan STATE: Virg: COUNTRY: Ung: COUNTRY: Ung: COUNTRY: Ung: COMPUTER READAI MEDIUM TYPE: COMPUTER: II OPERATING SYS SOFTWARE: PECURRENT APPLICATION PETLING DATE:	475 encent	1007 849 1067 886	947	832 725 888 782	772 671
CLASSIFICATION: 514 RIOR APPLICATION NUMBER: FILING DATE: 23-OCT- XIOR APPLICATION NUMBER: FILING DATE: 23-OCT- XIOR APPLICATION NUMBER: FILING DATE: 23-OCT- XIOR APPLICATION NUMBER: FILING DATE: 04-APR- XIOR APPLICATION NUMBER: FILING DATE: 04-APR- XIOR APPLICATION NUMBER: FILING DATE: 14-WAR- TONNEY, TAGENT INFORMAT: FILING DATE: 14-WAR- TONNEY, TAGENT INFORMATION INFORMATION INFORMATION TELEFAX: (703) 836-21		53 53 53 53 53 53 53	TTPTPRKM     : LGPVPHR- LLRPHVFM	TKKTI	PDE:     PAEE: ETTT	TTSD    -TSP
FICATION. PLICATION UDMI ATION NUME DATE: 23 PLICATION NUME ATION NUME PLICATION OF	ONDENCE ADDR SSEE: BURNS T: P.O. Box Alexandria RY: United (TYPE: Flor FING SYSTEM: APPLICATION UNMBER JOATE: 07	37A-5 5, Applicatic 5, S861381 INFORMATION: ANT: CLAMBOV ANT: KIENY ANT: LATHE ANT: HAREUYE OF INVENTION: OF INVENTION:	TTPTPRKMTSTMPELNPTS	TTTTE:	PDE:-STPEL	DKPAPTTPKETAPTT
ION: 514 NUMBER: NUMBER: 23-OCT- FION DATA: NUMBER: 23-OCT- FION DATA: NUMBER: 23-OCT- FION DATA: NUMBER: 14-MAR- INFORMAT NUMBER: NUMBER: NUMBER: 14-MAR- INFORMAT NUMBER:	DDRE RNS, BOX Tia ad s ad s ad s bd s bd s PC PC PC PC PC PC PC PC PC PC PC PC PC	iii d z 6	STMPE    PP EVTPDI	IMNKP	LSAEF    SP TKETA  :	TPKET     TFKPG
0 1 8 B H E T C " L C " L S " " L L L "	B ADDRESS: B BURNS, DOANE, S O. BOX 1404 andria ginia finited States -1404 ABLE FORM: Floppy disk IBM PC compatibl YSTEM: PC-DOSyM PatentIn Release CATION DATA: NUMBER: US/08/ 107-JUN-1995	n US/084 n US/084 n US/084 n US/084 marie-pare pharma pharma TREATM	PELNPTSRIAE       :    PPFEPGSAVA- PDMDYLP 108   :    Herypp 902	EEKER	STPELSAEPTPKALENS-	APTTE
PER 90/1: 1990 1990 1991 1991 15 08/03 15 08/40 1993 100: 15 08/40 1995 100: 15 08/40 1995 100:	DOANE, SW 1404 1404 ttates ttates ttates py disk py disk py disk py disk py disk py disk pp disk py disk po po p	n US/08479537A  , Pierre Marie-Paule Richard NI, Mara PHARMACEUTICAL TREATMENT OR P	PRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHM	TKKTITTEIMNKDEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK EKEREREREKEREREKERELERSVKLAQEGRAPVECPS	PDE:-STPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTP	
3101 FR91, 39, 3; 39, 3;	SWECKER &	37A TICA	MLQTT    T	TNSKA	-PKEPO      PKVVI	KEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTK
/00835 /6 025	ve ve	72	TTRPNOTPNSKLVEVN 	VTTPKI	PKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTP	KPAPT  : GPS-G
-	in	COMPOSITION OF	TPNS:  ::  GPDT	POKPT :: ERELE	KTPAA : :  ASQSA	TPETF     LPSLF
	*1.3	OF	KLVEV ; PALRT	KAPKK ::   RSVKL	TKPEN: RFNKI	Wdddd
	L.P.	FOR T	NPKSEDA      LSEYA	PTSTK	MTTTAI HLDRGI	SEVST
		R THE	EDAGGA	KPKT	KDKTT : FNSCA	PTTTK   : PPLS-
		T TUMOR	AEGET	MPRVR	ERDLF    RSDLY	EPTTIHKS
		ÖR .				
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Best Local Similarity 23.7
Matches 255; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
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LOCATION: 128..1727
OTHER INFORMATION: /r
OTHER INFORMATION: 12
OTHER INFORMATION: 20
OTHER INFORMATION: re
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 291
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OTHER INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                  376 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 422
                                                                                                                                                                                                                                                                                                  123 -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                    335 TTPKEPAPTTT-----KSAPTTPKEP-----APTTTKEPAPTTPKEPAPTT 375
                                                                                                                                                                                                                                                                                                                                                                                                   292 P-KAETTIKGP--ALTIPKEP------TPTIPKEPASTIPKEPIPTIKSAP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                      66 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
                                   360
                                                                                                                                                                                                                                    APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                PAPTTPKEPAPTTPK - - - - KPAPTTPKEPAPTTPK - - - - EPAPTTTKKPAPTAPKEPAPT
                                                                                                  APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 359
                                                                                                                                  TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
                                                                                                                                                                                                  PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 469
                                SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
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144
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134
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147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 424.5; DB 2
23.7%; Pred. No. 4.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acid 134 is x1 = xaa which is the codon for Pro or Ala wherein Pro = CCT, CCC, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr =
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acids 1 to 21 are a
21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 241;
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                                                                                                                                                                                                                                                240
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                                                                                                                                              518
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RESULT 13
US-09-083-116-5
; Sequence 5, Application US/09083116
; Sequence 5, Application US/09083116
; Patent No. 6203795
GENERAL INFORMATION:
    APPLICANT: CHAMBON, Pierre
    APPLICANT: LATHE, Richard
    APPLICATION OF A MALIGNANT TUM
    TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUM
    APPLICATION OF A MALIGNANT TUM
    STREET: Po. BOX 1404
    CITY: Alexandria
    STATE: Virginia
    COUNTRY: United States
    ZIP: 22313-1404
    COMPUTER: LBM PC compatible
    COMPUTER: LBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION UMBER: US/09/083,116
    FILING DATE:
    CLASSIFICATION DATA:
    PRIOR APPLICATION DATA:
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08/479,537

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FEATURE:

NAME/KEY: Peptide

LOCATION: 1..21

OTHER INFORMATION:

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Best Local Similarity 23.7%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
TYPE: amino acid
STRANDEONESS: single
TOPOLOGY: linear
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FILING DATE: 23-0CT-1991
PRIOR APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-193
PRIOR APPLICATION NUMBER: US 08/039,320
FILING DATE: 14-ARA-195
PRIOR APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-195
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
123 --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                              335 TTPKEPAPTTT-----KSAPTTPKEP---
                                                                                                          292 P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTFTTIKSAP 334
                                                                                                                                                                          233 TSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 291
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LOCATION: 128..1727
OTHER INFORMATION: OTHER INFORMATION: 11
OTHER INFORMATION: 22
OTHER INFORMATION: 21
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                                                                                                                                                                16 TVLTV-----
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                                                                        PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
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147
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                                                                                                                                                  ---VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
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21 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Thr or Asn wherein Thr = ACT,
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acid 134 is x1 = xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
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                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                          Score 424.5; DB 4; Length 1867;
Pred. No. 4.2e-19;
9; Mismatches 511; Indels 241;
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precursor s
                                      ----- APTTTKEPAPTTPKEPAPTT 375
                                                                                                                                                                                                                                                                                                                                             o 21 are a sequence."
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GENERAL INFORMATION:
APPLICANT: CHAMBON
APPLICANT: KIENY,
APPLICANT: LATHE,
APPLICANT: HAREUVE

CHAMBON, Pierre KIENY, Marie-Paule LATHE, Richard

CHAMBON,

APPLICANT: HAREUVENI, MARA TITLE OF INVENTION: PHARMAC TITLE OF INVENTION: TREATME

PHARMACEUTICAL COMPOSITION TREATMENT OR PREVENTION OF

FOR THE A MALIGNANT TUMOR

Sequence 2, Application US/08479537A Patent No. 5861381

958 VTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPD	Db
1101 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGTPSPTD	Qy
912 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTA	Ф
1042 - PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD	Qy
869 -GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPX	Dβ
982 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAFAMLOTTTRPNOT	Qy
821 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRDXP-	B
922 TTTQDTTPEKITTLKTTTLAPKVTTTKKTITTEIMNKPEETAKPKDPATNSKATTTEN	Qy
763 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	B
866 -TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTOVTS	Qy
703 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	Db
820 TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA	Qy
645 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	Вb
776 KPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP	Qγ
AHGVTSA	Дb
730 KEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTGTTSD	Qy
531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS	망
682 TTPKKPAPKELAPTTTKEPTSTTSDXDTTDXCATATIONSTATES	Qy
472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS	Db
627 TPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP	Qy
420 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGST	В
571 TPKETAPTTPKKLTPTTPEKLAPTTDEKDARTTBEFFF	γO
360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT	Db
519 PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPT	Qy
301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT	DЬ
470 TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTK	Qy
241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	DЪ
423 PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTT	Qy
181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	DЬ
376 TKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTT	Qy

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CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: FR 90/13101

APPLICATION NUMBER: FR 90/13101

FILING DATE: 23-OCT-1990

PRIOR APPLICATION NUMBER: WO PCT/FR91/00835

APPLICATION NUMBER: WO PCT/FR91/00835

APPLICATION NUMBER: US 08/039,320

FILING DATE: 04-APR-1993

PRIOR APPLICATION NUMBER: US 08/403,576

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

NAME: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: WOTHER INFORMATION: WOTHER INFORMATION: OF DESTURE:
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LOCATION: 128.1899 ...
OTHER INFORMATION: /not
OTHER INFORMATION: 128
OTHER INFORMATION: 20 ...
OTHER INFORMATION: repe
FEATURE:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide LOCATION: 134
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United
ZIP: 22313-1404
                                                                                                                                                               NAME/KEY: Peptide LOCATION: 147
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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NAME/KEY: Peptide LOCATION: 1..21 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acid 134 is X1 = Xaa Xaa which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                          /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = CCT, CCC, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn wherein Thr = or ACG; and Asn = AAT or AAC."
   /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
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US-08-479-537A-2

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RESULT 15
US-09-083-116-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UMBER: WO PCT
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
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                                FEATURE:
NAME/KEY:
LOCATION:
OTHER INFOR
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                                                                                             NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION: 17
OTHER INFORMATION: 17
OTHER INFORMATION: 20
OTHER INFORMATION: re
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/083,116
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/039,320 FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/403,576
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APPLICANT: HAREUVENI, MGRA
TITLE OF INVENTION: PHARMACEUT
TITLE OF INVENTION: TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
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                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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CITY: Alexandria
STATE: Virginia
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                INFORMATION:
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P.O. Box 1404
                                                               Peptide
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ID NO: 2:
                                                                             /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
     /note= "Amino acid 134 is X1 = Xaa Xaa which is the codon for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO PCT/FR91/00835
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   or Ala wherein
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645 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS-.-TAPXAHGVTSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                 730
                                                                                                                                                  531
                                                                                                                                                                                  682
                                                                                                                                                                                                   472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
                                                                                                                                                                                                                                                                                                      571 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
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                                                                                                                                                                                                                                                                                                                                                       360
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                                                                                                                                                                                                                                                                                                                                                                                                                                          470 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK---E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 TTPKEPAPTTT-----KSAPTTPKEP------APTTTKEPAPTTPKEPAPTT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                     TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
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                                             KPAP - - TTPK - - -
                                                                 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                        KEPAPTTPKG----TAPTTLKEPAPTTP---
                                                                                                                                  TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR 585
                                                                                                                                                                  TTP-----KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 729
                                                                                                                                                                                                                                                                      SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                                                                                                                                                                                                                                                                                                       SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 419
                                                                                                                                                                                                                                                                                                                                                                       PAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTTKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                         APDXRP-XPGSTAPXAHGYTSAPDXRPXPGSTAPXAHGYTSAPDXRPXPGSTAPXAHGYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP
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147
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Pred. No. 4.6e-19;
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                                  ----KKPAPTTPETPPPTTSEVSTP
                                                                                                 ---KKPAPKELAPTTTKGPTSTTSD
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180

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Gaps

53;

65

Search completed: April 26, 2002, 16:25:33 Job time: 473 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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         Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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6814
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T31108
S499178
S499178
S499178
F130826
F130826
F1365025
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A54641 A43427	A45155 T31113	A37221 T45463	S70795 T45462	T32271	A47282	QFMSH JH0557	S20500 T27642 JU0465
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## ALIGNMENTS

A;Reference number: A3532; MUID:89197956 A;Accession: B31532 A;Molecule type: mRNA A;Residues: 1916-2193 <gu4> A;Cross-references: GB:M22405; NID:9188873; PIDN:AAA36334.1; PID:9188874 A;Experimental source: intestine R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.</gu4>	A; Accession: A43932 A; Molecule type: DNA A; Rosidues: 1343-1350, 'L',1352-1411, 'S',1413-1448, 'P',1450-1503, 'T',1505-1915 <tor> A; Cross-references: GB.M74027; NID:918863; PIDN:AAA59875.1; PID:918864 A; Note: sequence inconsistent with the nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750) R; Gum, J.R; Byrd, J.C; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S. Biol. Chem. 264, 6480-6487, 1989 A; Title: Molecular Cloping of human intention</tor>	A; Status: not compared with conceptual translation A; Science type: mRNA A; Residues: 2037-3020 <803> A; Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398 A; Experimental source: colon A; Note: sequence extracted from NCBI backbone (NCBIP:116598) A; Note: sequence extracted from NCBI backbone (NCBIP:116598) A; Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, J. Clin. Invest. 88, 1005-1013, 1991 A; Tele: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym A; Reference number: A3932. WITH, 0156717	J. Biol. Chem. 267, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S. J. Biol. Chem. 267, 21375-21383, 1992 A;Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both up   A;Reference number: A45106; MUID:93016075 A;Accession: A45106 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 626-1895 <guz> A;Cross-references: GB:M94131; NID:9186395; PIDN:AAA59163.1; PID:9186396 A;Note: sequence extracted from NCBI backbone (NCBIP:116706)</guz>	RRSULT 1 A43932 mucin 2 precursor, intestinal - human (fragments) N;Alternate names: mucin SMUC-41 C;Species: Homo sapiens (man) C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999 C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S. J. Biol. Chem. 269, 2440-2446, 1994 A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of t. A;Reference number: A49963; MUID:94132002 A;Accession: A49963 A;Molecule type: mRNA A;Residues: 1-639 <gui>A;Cross-references: GB:L21998 B;Cross-references: GB:L21998</gui>

```
J. Clin. Invest. 87, 77-82, 1991
A; Fitle: Human bronchus and intestine express the same mucin gene.
A; Reference number: A61257; MUID:91086481
A; Recession: A61257 MUID:91086481
A; Accession: A61257
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 'T',1925-1948, 'TTS',1952-1954 <JAN>
A; Residues: 'T',1925-1948, 'TTS',1952-1954 <JAN>
A; Experimental source: bronchus
B; Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; R; Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; R; Xu, G.; Huan, Intestinal mucin-like protein (MLP) is homologous with rat MLP in A; Reference number: PQ0328; MUID:92198477
A; Accession: PQ0328; MUID:92198477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: P00329
A;Molecule type: protein
A;Residues: 2328-2342,'K',2344-2354 <XUG1>
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A; Residues: 2328-2468 <XUG>
A; Cross references: GB:M86523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: GDB:MUC2
A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von C;Superfamily: von Willebrand factor type C repeat C;Keywords: 9lycoprotein; intestine; tandem repeat C;Keywords: 9lycoprotein; on Willebrand factor type C repeat homology <VWC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1184 ADKCGCYVEDTHYPPGASVPTEETCKSCVCTNSSQVVCRPEEGKILNQTQDGAFCYWEIC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1356 QCDVSVGFICKNEDQFGNGPFGLCYDYKIRVNCCWPMDKCITTPSPPTTTPSPPPTTTT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1244 GPNGTVEKHENICSITTRÞSTLTTFTTITLÞTTÐ-----TSFTTTTTTTTTTFTSSTVL 1295
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                                                                                                                                                                                                                                                          325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 CKGRCFE------SFERGRECDCDAQCKKYDKCCPDYESFCAEVKDNKKNRT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 KKK-----PTPKPP-----KVT 100
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                                                                                                                                                                                                      PPTTTPSPPTTTPITP-PTSTTTLPPTTTPSPPPTTTTPPPTTTPSPPTTTTPSPPTIT 1592
                                                                                                                                                                                                                                                        PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTT 384
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PTTTPSPPTTTTPSPPTTTTPPPTTTPSSPITTTP--SPPTT----TMTTPS--PTTT 1704
                              APTTPKEPAPTTPKEDAPTTTKKPAPTAPKEPAPTTPKETAPTTPEKLAPTT 502
                                                                                                   TTTPPPTTTPSPPTTTTTPPPTTTPSPPTTTPTTPPTSTTTLPPTTTPSPPPTTTTTPP 1652
                                                                                                                                    PKEPAPTTTKSAP-TTTKEPAPTTTKSAP-TTPKEPAPTTPKEPAPTTPKKP 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.6%; Score 1065; DB 2; Length 3020; 28.7%; Pred. No. 2e-39; tive 79; Mismatches 464; Indels 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------KAPTSKVLAKPTPKAETTTK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is homologous with rat MLP in the C-
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2-0ct-1333 #cevr_cmm3c +2	AEGEVENDLE	MTSTMPELNPTSRIAEAMLOTTTRPNOTP       :	TLEEYNWSCPSTPSKDRATUSKATTPKPOK	DTTPPKITTLKTTTLAPKVTTTKKTI 8      ::        ::    T:        ::    TPTPTPLSTBSIIRTTGLRPYPSSVLICC 2 TAKPKDRATNSKATTPKPQK 8  QENETWHICDEM-ATCKYNNTV    QENETWHICDEM-ATCKYNNTV    QENETHWHICDEM-ATCKYNNTV	TKPEMTTTAKDKTTERDLRTTPETTTAAP 8	PTTSEVSTPTTTKEPTTIHKSPDE 7	KELAPTTTKGPTST-TSDKPAPTTPKETA 6 :	PSDKPAPT-TPKGTAPTTPKEPAPT 6:	VSYGLICKNEDQKPGGVIPMAFCLNYEINVQCCECVTQPT 10  TTTTKEPTSTTSDKPAPT-TPKGTAPTTPKEPAPT 6	**************************************
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51;

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T31108
T31108
Cyst germination specific acidic repeat protein precursor - Phytophthora in C:Species: Phytophthora infestans (potato late blight agent)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T31108
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submitted to the EMBL Data Library, April 1998
A;Reference number: 220986
A;Accession: T31108
A;Accession: T31108
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1489 <GOE>
A;Cross·references: EMBL:AF061185; NID:g3851513; PID:g3851514; PIDN:AAC72308.
A;Genetics:
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A; Reference number: Z18485
A; Recession: T16251
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1274 < LEI>
A; Cross-references: EMBL: U46675; NID:g1166613; PID:g116621; PIDN:AAB52641.1; GSPDB:GNOC
A; Experimental source: strain Bristol N2; clone F35A5
C; Genetics:
C; Genetics:
A; Map position: X
A; Introns: 1272/2
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hypothetical protein F35A5.1 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
c;Date: 10-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
c;Accession: T16251
C;Accession: T16251
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                                                                                                                                                                                                                                                                             394
                               349
                                                                   573
                                                                                                                                                                         265
                                                                                                                                                                                                                                                                                                                                                                                                                                                71 KNRTKK-KP-----TP-----KPPVVDEAGSGLDNGD----FKVTTPDTSTTQHNKVSTS 115
633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTEETTYAP----TEETTYEPTEE 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VPTTKTPAATKPEMTTTAKOKTTERDLRTTP----ETTTAAPKMTKETATTTEKTTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTEETTYEPTGETTYAPTEETTYAPTEETTYAPMEETPYEPAEESTSTVSTEKPCNTEEF 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEETTYAPTEATTYAPTEETPYA 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KITATTTQVTSTTTQDTT------PFKITT---LKTTTLAPKVTTTKKTITTTEIM 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDEPTDEPTDE--PSDEPTDEPTDEPTDLPTDEPSTPCDNQGINGIGVENKVRYNNAG 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP--NQTPNSKLVEVNPKSEDAG 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKPEETAKPKDRAT -- NSKATTPKP-QKPTKAPKKPT----
                                                                                                                                                                                                                                                                            PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP
                                                                                                                                                                                                                                                                                                              ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA----
                                                                                                                                                                                                                                                                                                                                               SPVVPPTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPS
                                                                                                                                                                                                                                                                                                                                                                            PKITTAKPI-NPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 174
                                                                                                                                                                                                          EAPAKKTPVLKRKEPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPA-
                                                                                                                                                                                                                                         KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290;
                                                                                                                                     TPVKNPVKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKP
APTAPKKPAP-----TTPKEPAPTTPKEPAPTTTKEP----SPTTPKEPAPTTTKSAPT 398
                                                                 RDPSPKKVAPTAPEKKTPVLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVPAKPVPKTEV
                                                                                                KEP----APTTPKKPAPTTPKE----PAPTTPKEPTPTTPKEPAPTTKEPAPTTPK-EP
                                                                                                                                                                         TTTKEPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 802; DB
Pred. No. 2.9e
02; Mismatches
                                                                                                                                                                           --PTTPKEPAPTTTKEPAPT----TTKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
2.9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -STKKP-KTMPR 908
                                                                                                                                                                                                                                                                                                                      ------LTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              333
                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                            393
                                                                              632
                                                                                                                 348
                                                                                                                                                   572
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                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                    298
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	1244 ADFTMPAPKKPDTEDP 1259	Db 1
	914TTPTPRKMTSTMP 926	Qy
1040		Db 1:
913	863 IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK	Qy
1193	1	pb 1:
862	TTTE	Qy 8
1149		Db 10
802	764 VPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPK	Qy 7
F 00 T		Db 10
763		0у 7
1031		Db 9
711		Оу б
9/4		Db 9
658		Qy 6
918	866 PSPKKAEPNSPVVPPTPVKNPVKKW-KPPWEDDDEPTEEVKKPSEPEKKTPVLA	Db 8
620	562 PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP (	0у 5
800	806 PAEPVNVPEPEKKTPVLAKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKPEFVSKPKE (	Db 8
065		Ωу 5
	751 TEVPPAVVKKPEPVAKSRDPSPKKAK-AEPNSPVVPPTPVKNPVKKMKPFWEDDDA	Db 7!
007	454 TPKEPAPTTTKKPAPTA-PKEPAPTTPKETAPTTPKKLTPTTPKKLAPTTPEKEK 30/	ОУ 4
1		Db 69
750	:	
453		

C; Species: Saccharomyces cerevisiae C; Date: 10-Sep-1999 #sequence\_revision C; Accession: S48478; A26877; B26877; S2 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein RESULT S48478 A; Molecule type: DNA
A; Residues: 1-1367 <ROW>
A; Residues: 1-1367 <ROW>
A; Cross-references: GB: Z47047; EMBL: Z38061; NID: g603997;
A; Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
J. Bacteriol. 169, 2142-2149, 1987
A; Title: Gene fusion is a possible mechanism underlying A; Reference number: A91831; MUID: 87194600
A; Reference number: A91831; MUID: 87194600
A; Accession: A26877 R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478 A; Molecule type: DNA A; Residues: 1-242 <YAM> A; Cross-references: EMB A; Accession: B26877 A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; R;Pardo, J.M.; Tanez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A; Molecule type: DNA A; Residues: 762-1331 <YA2> A; Accession: S48478 EMBL:M16164; NID:g172522; PIDN:AAA35014.1; on 10-sep-1999 s27281; JC6123 NID:g603997; PID:g763364; GSPDB:GN00009 #text\_change 12-Nov-1999 the evolution of STA1 PID:g172526 PID:g172525

YIR01

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A; Nolecule type: DNA
A; Residues: 1-31 <PAR>
A; Residues: 1-31 <PAR>
A; Residues: 1-31 <PAR>
A; Cross references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R; Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.
A; Cross references: Coloration of the protein that is regulated by Mss10, is critical for pseudohy
A; Cross reference number: JC6123; MUID:g6323237
A; Reference number: JC6123; MUID:g6323237
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1367 <LAM>
A; Residues: 1-1367 <LAM>
A; Residues: 1-1367 <LAM>
A; Cross references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
C; Genetics:
A; Genetics:
A; Gene: SCD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A; Cross references: MIPS:YIR013c; SGD:S0001458
C; Superfamily: Yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
F; S-21/Domain: transmembrane #status predicted <TM1>
F; 1350-1366/Domain: transmembrane #status predicted <TM2>
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A;Title: Similar short elements in the 5'
A;Reference number: S27281; MUID:89031230
A;Accession: S27281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local :
730 TESSSAPVPTPS-SSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE 788
                                                                                                                                                                                            623
                                                                                                                                                                                                            482 TAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT-TPEEPTPTTPEEPAP-----TTP 535
                                                                                                                                                                                                                                                     567 TPVTSSTTESSSAPVPTPSSSTTESSSAPVPT----PSSSTTESSSAPAPTPSSSTTESS 622
                                                                                                                                                                                                                                                                                                                       427
                                                                                                                                                                                                                                                                                                                                         508 SSAPVPTPS-SSTTESSSAPAPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 VETKETTTINKOTSTOGKEKTTSAKETOSIEKTSAKDLAPTSKVLAKPTPKAETT--TKG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 TSSTSESSTTTSSTSESSTSSSTTAPATPTTTSCTKEKPTPPTTTSCTKEKPTPPHHDTT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 DLSTGCNNYDNQGHSQTDFPGFYWNIDCDNNCGGTKSSTTTSSTSESSTTTSSTSESSTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 DCDAQCKKYDK---CCPDYESFCAEVK-DNKKNRTKKKPTPKPPVVDE---AGSGLDNGDF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 313; Conserv
                                      APKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAP---TTPKEPAPT-TPKGTAPT 650
                                                                                   SSSAPVT----SSTTESSSAPVT----SSTTESSSAPVPTPSSSSTTESSSAPVPTPSSST
                                                                                                            KAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPT-TPKGTAPTTLKEPAPTTPKKP : || || : | || : | ||
                                                                                                                                                                     SAPVT----SSTTESSSAP-VPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE
                                                                                                                                                                                                                                                                                              AP----TTPKEPAPT-TPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKE 481
                                                                                                                                                                                                                                                                                                                                                                                  EPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAP----TTTKSAPTTPKEPSPTTTKEP
                                                                                                                                                                                                                                                                                                                                                                                                                             ESSSAPVPTPSSSTTESSSAPVT---STTESSSAP-VPTPSSSTTESSSAPVTSSTTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APTTPKEPTP---TTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP----TTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TESSSAPVTSS----TTESSSAPVTS---STTESSSAPVT----SSTTESSSAPVTSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVTSSTTESSSAPVPTPSSSTTESSSAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALTTPKE-----PTPTTPKEPASTTPKEPTPTTIKSAP----TTPKEPAPTTTKSAPT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCTKKKTTTSK-TCT---KKTTTPVPTPS-SSTTESSSAPV-----PTPSSSTTESSSA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVTTPDTSTTQHNKVSTSPKITTAKPINP-----RPSLPPNSDTSKETSLTVNKETT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 798.5; DB 1; 27.9%; Pred. No. 4.5e-28; tive 108; Mismatches 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions of the STA2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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				lase	udohy	cchar
	Query Matches Qy 78 Qy 78 Db 460 Qy 134 Db 511	RESULT S49915 extensin- C;Species C;Date: 0 C;Accessi R;Rubinstted A;Descrip A;Referen A;Referen A;Rocessi A;Status: A;Residue A;Crosser	Db 1 Qy Db 1 Qy 1 Db 1	Qy Db Qy Db 1	Qy Db Qy	Qy Db
SPPPPVKSPPPAPTTTKGPA  TTTKSAPTPKEPAPTTT    ::  PPTTKSAPTPKEPAPTTT    ::  PPTTKSAPTPKEPAPTTT    ::  PPTTKSAPTPFKEPAPTT    ::  PPTTTKSAPTPF	: EMBL: 234465; NID: 9600117; PIDN: CAA84230.1; PID: 9600  11.5%; Score 784; DB 2; Length 1188;  9nservative 59; Mismatches 359; Indels 122; Gapta 122; Ga	like protein - maize : Zea mays (maize) 5-Mar-1995 #sequence_re) on: S49915 ein, A.L.; Broadwater, i to the EMBL Data Libra- tion: Pax genes: pollen- ce number: S49915 on: S49915 preliminary e type: DNA sfarence	077 PSVTTVINFTPTT-ITTTVCSTGTNSAGETTSGCSPKTVTTTVPC 978 HVFMPEVTPDMDYLFRVPNOGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFW 1 :		706 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPK 760     :	651 TLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTP 705

_	Qy 164 TDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTIKGPALITIFTKAETTIKGPALITIFTKAETTIKGPALITIFTKAETTIKGPALITIFTKAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAETTIKGTAE	
	QY 112 VSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVEIKETITING 150  9 112 VSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVEIKETITING 150  1 1	
	GSGLDNGDFKVTTPDISTICHNK	
	; ; Ga	
	A;Gene: Naca A;Gene: Naca A;Map position: 10 A;Map position: 10 A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding active A;Note: differential splicing; DNA binding; transcription factor	0 5 5 5 5 5
	A; Modecule type: DNA A; Modecule type: DNA A; Residues: 1-2187 < YOT> A; Cross-references: EMBL: U48363; NID: g1666688; PID: g1666689; PIDN: AAB18732.1 C; Genetics:	~ ~ ~ ~ ~ ~
<u> </u>	Yotov nes Du Title Refer Acces	ו דבי טיפי ימי ימי
	N;Alternate names: alpha-NAC procern C;Species: Mus musculus (house mouse) C;Spete: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999	aaaz
	RESULT 7 T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse	5 H Z
	1116	י ט
	747	o.
	QY 688 -TPKETAPTTPKEPAPTTPKKPAPTTPETPPTTSEVSTPTTKEPTTITKEPTTITKSPDESIFEL (**)	<u> </u>
	629 - KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAKELHAPTTINGFISTIONERS.	dd VQ
	583 LKEPAPTTPKKPAPKELAPTTTKEPTSITSUKEAFETENSKALL	ду Дъ
	524 PTTPEEPAPTITKAAAKNIEGE EGELEKUS	da YQ
	477 828	Qy db
	417 EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTTKKPAPTAFKEPAPT	ОУ
	357 APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAFTTTASFAFTASFAFTASFAFTTASFAFTASFAFT	д УО
	660	Дb

RESULT 8
A33175
My.Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episia N; Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episia N; Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episia N; Alternate names: breast carcinoma-associated DF3 antigen; core protein 1 precursor (PEN) N; Contains: mucin 1 precursor, epithelial mucin (PEN) N; Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor N; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Jun-2000 C; Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Jun-2000 C; Date: 35175; B35175; A35886; A35887; S10572; S40293; A36735; PX00666; S10218, C; Accession: A35175; B35175; A35886; A35887, S10572; S40293; A36735; PX00666; S10218, C; Accession: A35175; B35175; Gennissen, A.M.C.; Hilkens, J.

H

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A; Molecule type: mRNA
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057
A; Experimental source: gastric carcinoma cell
R; 2rihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner
FEBS Lett. 356, 130-136, 1994
A; Title: Tyrosine phosphorylation of the MUC1 breast cancer membrane phosphorylation phosphorylation of the MUC1 breast cancer membrane phosphorylation of the MUC1 breast cancer membrane phosphorylation phosphoryla
                                    A; Note: undetermined C; Comment: This prote
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-142, 'Q', '144-162, 'Q', '164-168 <ABE>
A; Cross-references: EMBL:M31823; NID:g181542; PIDN:AA
R; Masuzawa, Y; Miyauchi, T; Hamanoue, M.; Ando, S.;
J. Biochem. 112, 609-615, 1992
A; Title: A novel core protein as well as polymorphic
A; Reference number: JX0235; MUID:93123189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, March 1990
A.Reference number: $40293
A.Reference number: $40293
A.Reference number: $40293
A.Rolecule type: mRNA
A.Residues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',1039-1344
A.Cross-references: EMBL:X5229; NID:g37053; PIDN:CAA36478.1; PID:g37054
A.Cross-references: EMBL:X5229; NID:g37053; PIDN:CAA36478.1; PID:g37054
B.Chem. Siddiqui, J.; Kufe, D.
Blochem. Blophys. Res. Commun. 165, 644-649, 1989
A.Fille: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associ
A.Recession: A36735; MUID:90088473
A.Rocession: A36735
                                                                                           A; Contents: annotation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A; Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A; Rostedues: GB:J05582; NID:g189598; PIDN:AAA60019-1; PID:g189599
A; Note: GenBank entry HUMPANMU contains four fewer copies of the tandemly r.
Eur. J. Blochem. 189, 463-473, 191
Eur. J. Blochem. 189, 463-473, 191
A; Title: Human epithelial tumor antigen cDNA sequences. Differential splicing A; Reference number: S10571; MUID:90276413
A; Recession: S10572
A; Molecule type: mRNA
A; Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE>
A; Cross references: EMBL:X52229; NID:g37053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-19,29-992,1033-1344 <GEN>
A;Residues: 1-19,29-992,1033-1344 <GEN>
A;Cross-references: GB:J05581; NID:9188869; PIDN:AAA59876.1; PID:9188870
A;Note: GenBank entry HUMMUCAB includes one copy of the tandemly repeated
R;Lan, M.S.; Batra, S.K.; Q1, W.N.; Metzgar, R.S.; Hollingsworth, M.A.
J. Biol. Chem. 265, 15294-15299, 1990
A;Title: Cloning and sequencing of a human pancreatic tumor mucin cDNA.
A;Reference number: A35887; MUID:90368716
A;Saccession: A35887
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                       A; Accession: PX0066
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A;Title: Molecular cloning and expression of human tumor-associated polymorphic epithel A;Reference number: A35886; MUID:90368715
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A; Residues: 1-19,29-952,1033-1344 <LIG2>
A; Cross-references: GB: M32739; GB: J05288; NID: g182126;
A; Experimental source: splice form B
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A; Residues: 1-952,1033-1344 <LIG1>
A; Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1;
A; Experimental source: splice form A
A; Experimental source: splice form A
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A:Title: Episialin, a carcinoma-associated A:Reference number: A35175; MUID:90202794
A:Accession: A35175
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                      protein is length
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       tyrosine residues in the carboxyl-terminal ain is length polymorphic. Individuals may )
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ado, S.; Yoshida,
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       may have
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J.; Takao,
non-repetitive have between 21
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and 125
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A;Gene: GDB:MUC1; PUM
A;Gene: GDB:MUC1; PUM
A;Gene: GDB:MUC1; PUM
A;Gross-references: GDB:120705; OMIM:158340
A;Map position: 1q21-1q23
A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C;Superfamily: polymorphic epithelial mucin
C;Ksywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphic epithelial mucin
F;1-1344/Product: mucin 1 precursor, splice form A *status predicted <PREA>
F;1-62/Region: mucin 1 precursor, splice form B *status predicted <PREA>
F;1-19,29-32/Domain: signal sequence *link PREA *status predicted <SIGA>
F;1-19,29-32/Domain: signal sequence *link PREA *status predicted <SIGB>
F;1-19,29-1344/Product: mucin 1 precursor, splice form B *status predicted <PREA>
F;1-19,29-212,1033-1344/Product: mucin 1 precursor, epithelial tumor antigen splice
F;1245-1272/Domain: transmembrane *status predicted <TRM>
F;1046,1064,1118,1144,1222/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;1213/Binding site: phosphate (Tyr) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partial repeats. The repeat shown is defined by SmaI nuclease sites. C:Comment: Serine and threonine residues in the tandem repeat domain are extensively C:Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48 C:Genetics:
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Best Local
                                           654 EPAPTTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 T-SAPDT--RPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 P-KAETTTKGP--ALTTPKEP------KE 231
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                                                                              AP-PAHGVTSAPDTRPAPGSTAPPAHGVTS----APDTRPAPGSTAPPAHGVTSAPDTRP
                                                                                                                                  APTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTPKEPAPTTPKG---
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                                                                                                                                                                                                       HGVTSAPDTRPAPGSTAP
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-KKPAPKELAPTTTKGPTSTTSDKPAP--TTPK----ETAPTTP 697
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Pred. No. 1.6e-22;
8; Mismatches 472;
                                                                                                                                                                                                                                                                                                                                                     --EEPAP--TTPKA----AAPNTPKEPAPTTPK-
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Qy	Ф	Qy	Db Qy	Qу Дъ	Qy	Оу	Ques Best Mato	A; Acce A; Stat A; Mole A; Resi A; Cros	R;Shim J. Cell A;Titl A;Refe	RESULT T18535 high m C; Spec C; Date	Оу 1 рь 1	Qy .	ду в	Qy 8	Qy 7	Oy 7	Qy 6 Db 7	Db 6
316 EPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKE 3/1	P- 39	~	-	GPALTTPKEPTP-TTPKEPAS	ETQSIEKTSAKDL :     : :: -SQSAPKATV-EV		y Match 9.8%; Score 671; DB 2; Length 1151; t Local Similarity 25.9%; Pred. No. 1.5e-22; ches 284; Conservative 100; Mismatches 419; Indels 292; Ga	Accession: F18030 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Molecule type: mRNA Residues: 1-1151 <shi> Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1</shi>	R;Shimada, K.; Harata, M.; Mizuno, S. R;Shimada, K.; Harata, M.; Mizuno, S. J. Cell Sci. 110, 3031-3041, 1997 A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick A;Reference number: Z18955; MUID:9803440	RESULT 9 T18535 high molecular mass nuclear antigen - chicken (fragment) C;Species: Gallus gallus (chicken) C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999	1011 ICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPESPPS 1046 1 :			KAPKKPT    TAPPAHG	90 LRTTPETTTAAPKMTKETATITEKTIESKITATITQVTSTTTQDTTPFKIT 	741 ESTPELSAEPTEKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERD 789	698 KEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTT1HK5PU /40	56 APGSTAPPAHGVTSAPDTRPAPGSTAP-PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR

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                             955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PTTP-----KAAAPNTPKE-----EEPAPTTP----KAAAPNTPKE-----
                                                                                                                                                                                                                                                                                                                                              MGAATPPQTPSVGAATTP-QPSPM----GAATTLMSPMGAATTPQ---PSPMGAVTTQPP 859
                                                                                                                                                                                                                                                                                                                                                                                                      GGATOMSPMGAANTOMSPMGATTTOMSPMGAAATTOPSPMGAAATQVTATSAGNTMOVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PAPTTPKEPAPTTPKEPAPTTPKETAPT------TPKGTAPT----- 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSSPVASAMHAKVTPRPLPASPVPMAASPASLGPDAARVALATNAASPGAKPEAAGGNG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPVPLMALTPQPVTAQMVTQLAATKPSPIVPKASPK-ALMTPPPPPPPGLPRALAAAKLLG 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TETTSDKPAPTTPKKPAPKELAPTTTKEP-----TSTTSDKPAPTTP
                                                                                                                                                                                                                               PPPPIPPSPTAQTSPQPMSKSPPPDPPKAPSAAAQTSPAAHVANASPGV-TAVSPA---P 975
                                                                                                                                                                                                                                                                                        ----TSTTSDKP-APTTPKET---APTTPKEP---APTTPKKP-APTTPETPP----- 717
                                                                                                                  AP----TKAKRSSSSSSSSSSSSSSSSSSSSSSSSDSDSSSSSSESNPASPA--- 1077
                                                                                                                                           TPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAP 894
                                                                                                                                                                        IGVTEASPSADGARLSPGPTAATDGPKASPAATADVTEAATD--VTAAATAVPA----EA 1029
                                                                                                                                                                                                   EMTTTAKDKTTERDLRTTPETTTAAPKMT-KETATTTEKTTESKITATTTQVTSTTTQDT 834
                                                                                                                                                                                                                                                         PTTSEVSTPTTTKEPTTIHKSPDESTPEL--SAEPTPKALENSPKEPGVPTTKTPAATKP 775
                                                                                  KKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLOTTTRPNQTPNSKLV 954
                             EVNPKSEDAGGAEGE 969
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RYPOTHER RESULT F16F9.2 - Caenorhabditis elegans

C; Species: Caenorhabditis elegans

C; Species: Caenorhabditis elegans

C; Species: Caenorhabditis elegans

C; Accession: T25697

R; Fulton, B.

Submitted to the EMBL Data Library, August 1996

Submitted to the EMBL Data Library, August 1996

A; Description: The sequence of C. elegans cosmid F16F9.

A; Reference number: 220071

A; Reference number: 220071

A; Rocession: T25697

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-1229 <FUL>
A; Experimental source: Strain Bristol N2; clone F16F9

C; Genetics:

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A:Map position: X
A;Introns: 35/1; 361/1; 384/1; 482/2; 517/1; 971/1; 1021/2; 1179/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.8%; Score 670; DB 2; Length 1229;
Best Local Similarity 27.0%; Pred. No. 1.8e-22;
Matches 321; Conservative 98; Mismatches 382; Indels 390; Gaps
                   723 -VSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTEAATKPEMTTTA 781
        822 SATTETTTSEPST----TEST----
                                                         762 TTTVVAENIDEVTTTEKEKVVQTTPITTEKSTTQEETTTTTTTEKTTSKTTTEKPTTSE 821
                                                                                                                                              702
                                                                                                                                                       644 PKGTAPTTLKEPAPTTP----- 676
                                                                                                                                                                                        652 ITTE-----GSTTTEEPTTTAIFAEASTGIITTDEETTSTTSTTPEITSTKE--IVT
                                                                                                                                                                                                                                                       601 -EKTSTTKKA---STTEE--PTTTDEPTTTT---ESSTTGKATTPELSTTSEETTTTELK 651
                                                                                                                                                                                                                                                                            528 EEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPA 587
                                                                                                                                                                                                                                                                                                                        547 ENPTTTEOPTSTAESTTTALPETTEOTVTTEEPTTAEKSTATQ----KPTTTQESVST--
                                                                                                                                                                                                                                                                                                                                                      474 PAPTT---PKETAPTTPKKLTPTTPEKLA---PTTPEKPAPTTPEELAPTTPEEPTPTTP 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 APTTPKEPSPTTTKE---PAPT-----TPK-----EPAPTTPKKPAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 Р----КЕРАРТТРКЕРТ---РТТРКЕРАРТТКЕРАРТТРКЕРАРТАРККРАРТТРКЕРАР 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VSTTTEEPTTTAESTTKKSTTKAPATTEEPTPTTTEEVTTTEAETSTTTSSETSTEKPTT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 APTTTKEP---APTTPKE----PAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPA---PTT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 EQTSPONTTEIAS -- PMETNTTT -- EATTTSVEPSVSTLASEDETTVTAIAESTTTVIAE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 KEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKS------APTTPKEP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 KDSTTPEIITGIVVINSKSESVTDMSTTRFSTTLSPTTELLTSP----ETLVSTDSSTST 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AKPINPRPSLPPNSDTSKETSLTVNKETT-----VETKETTTTNKQTS---TDG
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                                                                                                                         ESAITOTSVSVVESSTPROLPERWKAIVNKFKHNLEVLKEKKRLLKEKESTSTTGSDSSE 761
                                                                                         -----TSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPE--TPPPTTSE 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AW-VVSFAFLILGNVVQSSSLLSKTINSDGSRDFKIVKHIKKNTCTCSC----KCVPD--
                                                                                                                                                                                                                      PTTPKKPAPKELAPTTTKEPTSTTSDKPAP----TTPKGTAPTTPKEPAPTTPKEPAPTT 643
                                                                                                                                                                                                                                                                                                                                                                                                                       2 AWKTLPIYLLLLISVFVIQQVSSQELSCKG-RCFESFERGRECDCDAQCKKYDKCCPDYE 60
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----TVDTSSATTEESSTAA
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	863 PPV	85		743 GR 232 PT	200 -K	683 AT	23	568 SS	70 K		Best Local s Matches 360  Y 19 1000	Oy 803 MTKE Db 912 KHKTI OY 856 KTITI OY 899 STKK Db 1022 I RESULT 11 T45025 mucin MUC5B, t: C;Species: Homo C;Date: 21-Jan C;Accession: TR;Desseyn, J.L. J. Biol. Chem. A;Title: Human A;Reference nun A;Reference nun A;Reference nun A;Reference nun A;Reference nun A;Residues: 1-3 A;Cross-referen A;Status: prelif A;Molecule type A;Residues: 1-3 A;Cross-referental C;Gene: MUC5B	782 855
STPALSSPHPSSRTTESPPSPGTTTPGHTTATSRTTATATATSKTRTSTLLPSQP 976	PVPNTTATTHGRSLSPSSPHTVCTAWTSATSGILGTTHITEPSTGTSHTPAATTGTTQH 922	PAPTTTKSP 314		GSMATPSSSTQTS	KAETTTKGPALTTPKEPTPTTPKEPASTTPKE 231	ATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTPGTAHTTKVLTTTTTGFTATPSSSD 743		PHVSTTATTPT		IDQV-GQVLTCSLETGLTCKNEDQTGRFNMCFNYNVRVLCCDDY-SHCPSTLAT 567	9.6%; Score 651.5; DB 2; Score 651.5; DB 2; Conservative 107; Mismatches 538; SSOPI-SCREPPERPERPERPERPERPERPERPERPERPERPERPERP	TATITEKTTESKITATTTQ-VTSTTTQDTTPFKITTLAFKVTTTK     :	KOKTTERDLRTTPETTTAAPK 802

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATPSSTPGTTWILTELTTTATTTESTGSTATPTSTLRTAP--PPKVLTTTATTPTVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTPPVPNTTATTHGRSLSPSSPHTVRTAWTSATSGTLGTTHITEPSTGTSHTPAAFTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AQAQPGVPLRELGQVVECSLDFGLVCRNREQVGKFKMCFNYEIRVFCCNYGHCPSTPATS
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                                                                                                                                                                                                                                                                                                                      SSKATSSSSPRTATTLPVLTSTATKSTATSFTPIPSSTLGTTGTSQNRPPHPMATMSTIH
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                                                                                                                                                                    TKKPKT---MPRVRKPKTTPTPRKMTSTMPELNPTSRIAEA--MLQTTTRPNQTPNSKLV 954
                                                                                                                                                                                                    TPSSTPGTTWILTEPSTTATVTVPTGSTATASSTRATAGTLKVLTSTATTPTVISSRATP
                                                                                                                                                                                                                      TTKKTITTEIMNKPEETA------KPKDRAT--NSKATTPKPQKPTKAPKKPTS
                                                                                                                                                                                                                                                              T--PPVWISTT----TTPTTRGS---TVTPSSIPGTTHTATVLTTTTTTVATGSMATPSS
                                                    CNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPSPARRI--
                                                                                   SSTPETVHTSTVLTTTATTTRIGSVATPSSTPGTAHTTKVPTTTTTGFTATPSSSPGTAL
                                                                                                                                             EVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVP---NQGIIINPMLSDETNI 1011
-TEVWGIPSPIDTVFTRCNCEGKT
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hypothetical protein ZK783.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Apecies: Caenorhabditis elegans
C; Accession: T34513
A; Reference number: Z21536
A; Reference number: Z21536
A; Accession: T34513
A; Accession: T34514
A; Accession: T345
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A; Residues: 1-3507 <FAV>
A; Cross references: EMBL: U13646; PIDN: AAC24418:1; GSPDB:GN00021;
A; Experimental source: strain Bristol N2; clone ZK783
C; Genetics:
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A;Map position: 3
A;Introns: 14/1; 48/2;
3504/1
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-APTTPKAAAPNTPKEPAPTT---
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949 FMSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDE 1008	Ş
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6883 KVEEKRIILPKEEEVLPVEVTEEPEE	Db
EIMNKPEETAKPKDRATNSKATTBKBOKBTKATKE	Qy
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69 EEEVLFEEEIVPEEEVLPEEEEVLPE-EEEVLPEEEEVPPEEEEVPPEEEYVP	₽ ₽
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TPEKPAPTTPEELAPTTPEEPT 5	Qy
KPVPEEPVPTKPKA	ДЬ
TTPKKPAPTTPKEPAPTTPKEPAPTTPKEPA	Qy
KERAYTLEEEAVSVOREEEVEEVEEVENVKERREGERVOOR	Db
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TVPEKKVPAPVPKKEKVPPPKVPEEPKKPVPKETTIKKEPAPTTYKSAP 3	Db
PAPTTPKEDAPTTPKED-ADPTTPKED-A	VQ
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28 VEEKREVAEEKLSFAVPORVEVTRHEVGAFEFWGVSEFFFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DЬ
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231 EPTPTTIKSAPTTPKEPAPTTTKSJ	3 5
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C; ACCESSION: 111044; 534135

NO. Plant Microbe Interact. 10, 95-101, 1997

NO. Plant Microbe Interact. 10, 95-101, 1997

A; Title: Rhizobia modulate root-hair-specific expression of extensir A; Reference number: Z17301; MUID:97155574

A; Reference number: Z17301; MUID:97155574

A; Reference number: Z17301; MUID:97155574

A; Residues: preliminary; translated from GB/EMBL/DDBJ

A; Accession: T1622

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-489 < ARS>
A; Cross-references: EMBL:X91836; NID:g1015936; PIDN:CAA62943.1; PID:A; Cross-references: EMBL:X86030; NID:g1015936; PIDN:CAA62943.1; PID:G1015936; PI
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C;Species: Vigna unguiculata (cowpea)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Accession: T11622; S54155
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C;Keywords: glycoprotein; hydroxyproline
F;1-23/Domain: signal sequence #status predicted <SIG
F;24-489/Product: extensin class 1 #status predicted
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Pred. No. 2.
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2.9e-21;
1es 252;
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
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A; Map
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A; Molecule type: DNA
A; Residues: 1-761 <STO>
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C;Genetics:
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Gene: At2g27380
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nes 217; Conserv
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648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPKAETTTKGPALTTP----KEPTPT-TPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPIKPPVHKPPTPIYSPPIKPPPVHKPPTPIYSPPIKPPPVHKPPTPTYSPPVKPPPVHK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPKKP---APTTPKEPAPTTP----KEPTP--TTPKEPAPTKEPAPT-TPKEPAPTAPK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPIQKPPTYSPPIYPPPIQKPPTPTYSPPIYPPPIQKPPTPTYSPPIYPPPIQKPPTPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSPPIYP----PPIQKPPTPSYSPPVKPPPV---QMPPTPTYSPPIKPPPVHKPPTPTYS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                              PPTPIYSPPIKPPPVHKPPTPIYSPPVKPPPVQTPTPTYSPPVKPPPVHKPPTPTYSPP
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                                                                                                                                                                                                                                                                                                                                                                                                               APTTPKEPSPTTTKEP---APTTPKEPAPT--TPKKPAPTTPKEPAPTTPKEPAPTTTKK 465
                                                                                                                                                                                                                   KETAPTTPKGTAPTTLKEPAPT--TPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAP
                                                                                                                                                                                                                                                       KLPPVKPPTPIYSPPVKPPPVHKPPTPIYSPPVKPPPVHKPPTPTYSPPIKPPPVKPPTP
                                                                                                                                                                                                                                                                                    ELAPTTPEEPTPTTPEEPAPT----TPKAAAP-NTPKEPAPTTPKEPAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                                                                     PTPIYSPPVKPPPVHKPPTPIYSPPVKPPPIQKPPTPTYSPPIKPPPLQKPPTPTYSPPI 420
                                                                                                                                                                                                                                                                                                                                         PAP---TAPKEPAPT----TPKETAPTTP----KKLTPTTPEKLAPTTPEKPAPTT----PE
                                                                                                                                                                                                                                                                                                                                                                                  VKSPPVQKPTPTVSPPIKPPPVQKPPTPTYSPPIKPPPVKPTPIYSPVKP-PPVHKP
                                                                                                                                                        TTPKEPAPTTPKEPAPT-TPKGTAPTTLKEPAPT--TPKKPAPKELAPTTTKGPTSTTSD
                                                                                                                            SPPIKP-PPVHKPPTPTYSPPIKPPPIHKPPTPTYSPPIKPPPVHKPPTPTYSPPIKPPP
                                                                                                                                                                                           TYSPPVQP---
                              DESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTA
                                                             VHKPPTPTYSPPIKP----PPVHKPPTPTYSPPIKPPPVHKPPTPTYSPPIKPPPVHKPP
                                                                                        KPAPTTPKETAPTTPKEPAPTTPKKPAPT-TPETPPPTTSEVSTPTTTK--EPTTIHKSP
-TPTYSPPIKPPPVQVPPTPTYSPPVVPPPVQLPP-TPTYSPPVVPPPVQVPPTPTYS
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                                                                                                                                                                                           -PPVQKPPTPTYSPPVKPPPIQKPPT----PTYSPPIKPPPVKPPTPTY
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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